#### FIGURE 1A

#### 20CAGHA

#### 127CAGHA

#### FIGURE 1B

20QHA MGGPPSTPQ<sub>20</sub>TSRTYPYDVPDYA

127QHA MGGPPSTPQ<sub>127</sub>TSRTYPYDVPDYA

Figure 1. A) DNA sequences of 20QHA and 127QHA and B) their predicted protein sequences. The protein-coding region is underlined. The Kozak sequence is in italic.

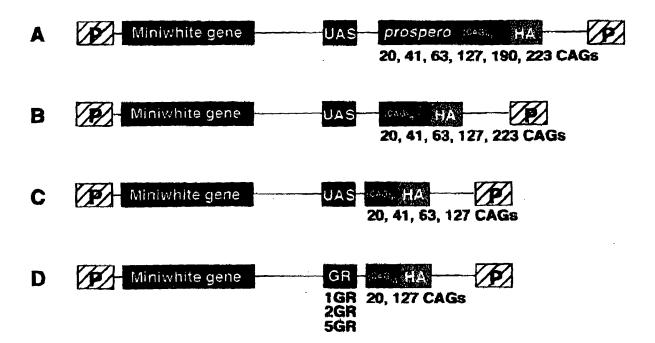


Figure 1. P-element plasmid constructs for production of transgenic flies. Each construct has two P-elements for chromosomal insertion. To facilitate identification of transformed flies, a miniwhite gene is included to produce red pigmentation in the eye. A) Plasmids carrying the full-length cDNA encoding the fly PROSPERO with various CAG repeat sizes. The expression of PROSPERO is regulated by five tandem upstream activating sequences (UAS). The yeast transcription factor GALA activates the transcription from these UAS elements. At its 3'-end, prospero cDNA is joined, in-frame, to a short DNA sequence that codes for a heterologous epitope, hemeagglutinin (HA). Antibodies against HA will be used to label the protein in immunohistochemical assays and Western blots. B) Plasmids carrying a partial cDNA encoding 422 amino acids of the C-terminal end of PROSPERO with various CAG repeat sizes. C) Plasmids carrying a DNA sequence that only encodes polyglutamines of various sizes. D) Plasmids carrying a DNA sequence that only encodes polyglutamines of various sizes, expressed under the control of one, two or five GLASS response elements (1GR, 2GR, or 5GR). The eye-specific protein GLASS activates the expression of polyglutamines from the GLASS response elements.

### Generation of the P-element insertion and screening for modifiers

```
M P[Δ2-3]/P[Δ2-3] X F EP55/EP55

M EP55/Y;; P[Δ2-3]/+ X F w/w

M w/Y;pEP/+;+ or w/Y;+;pEP/+ X F w;GMR/CyO;127Q/127Q

Progeny screened for eye phenotype

Isolation of the new P-element insertion (pEP = suppressor or enhancer)

M (GMR;127Q)/pEP X F (CyO;TM3)/Xa

M GMR/CyO;pEP/TM3 X F w1118

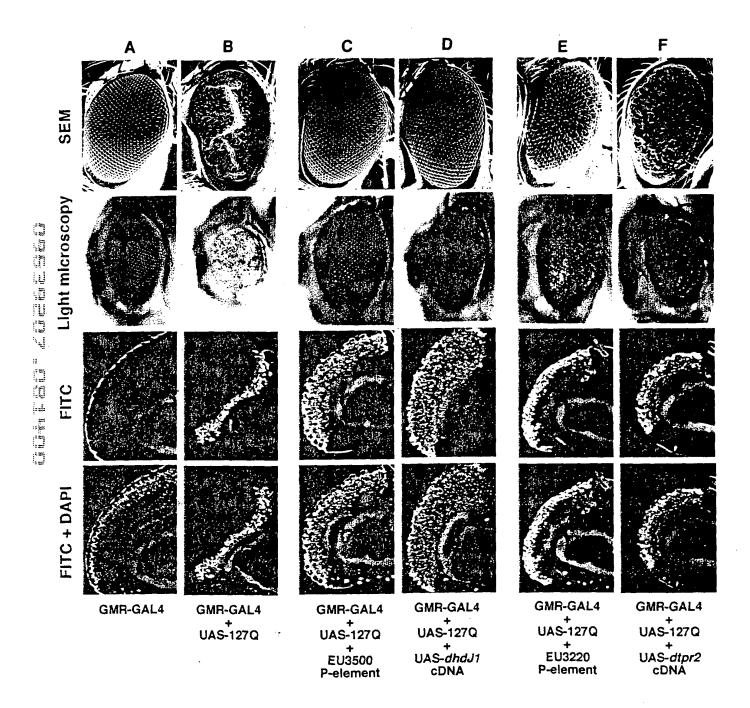
M GMR;TM3 or CyO;pEP X F w;GMR/CyO;127Q/127Q to test

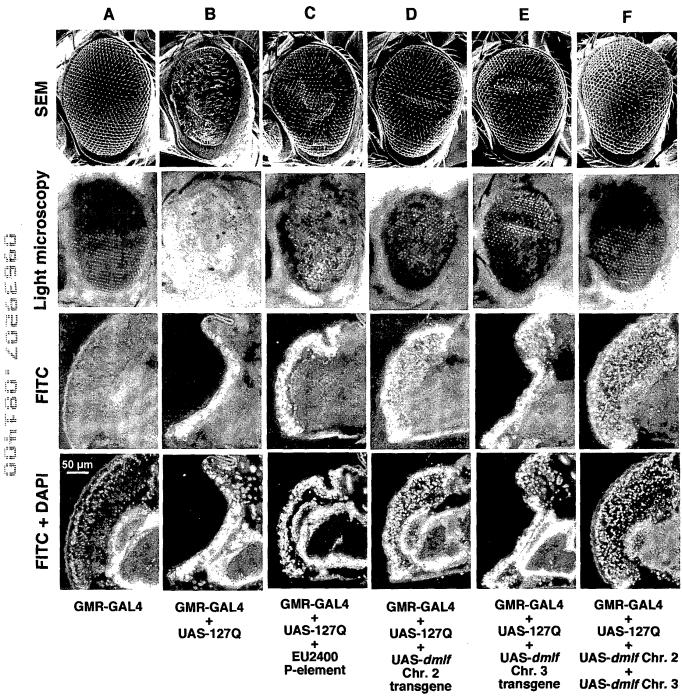
X F (CyO;TM3)/Xa to establish line

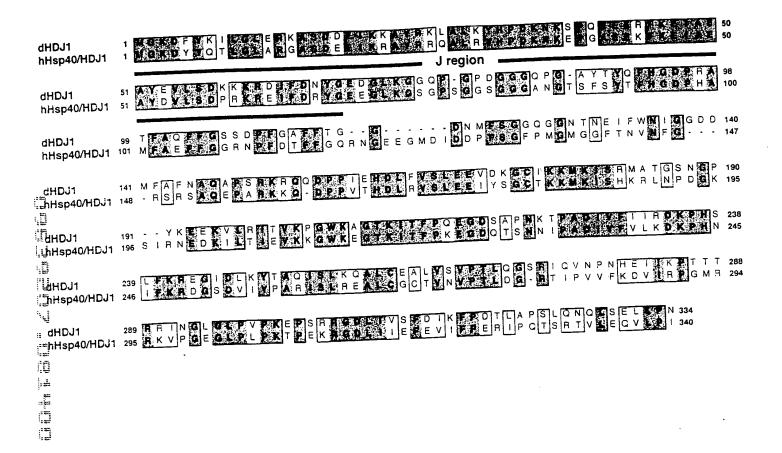
M +/CyO;pEP/TM3 X F +/CyO;pEP/TM3

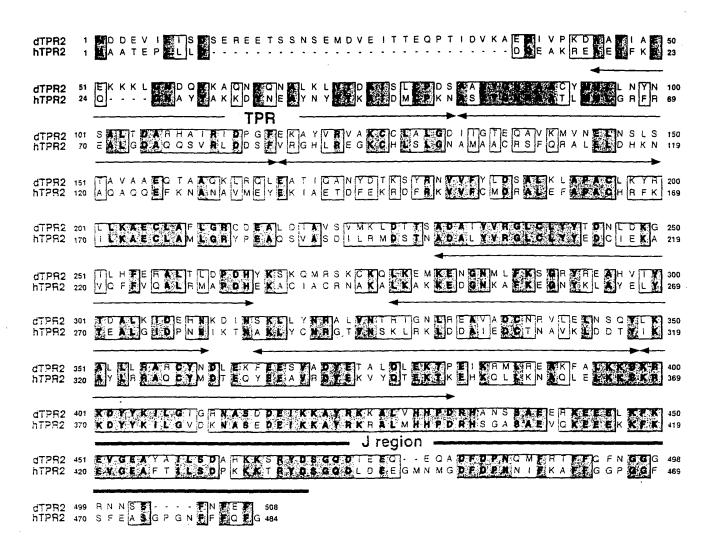
pEP/TM3 or pEP/pEP established lines
```

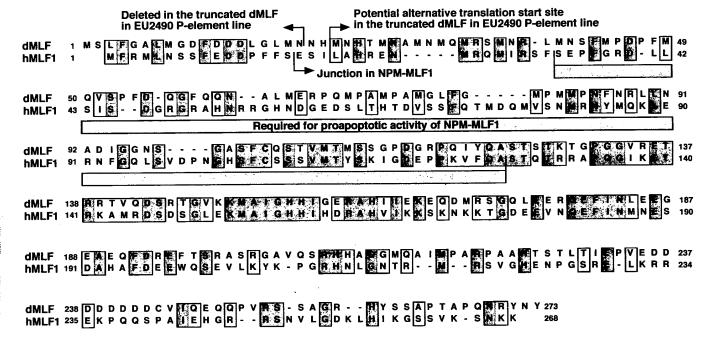
Genetic scheme used for generating P-element mutants, screening for modifiers of polyglutamine toxicity, and isolating a hypothetical modifier P-element insertion on chromosome 3. Homozygous EP55 virgin females were crossed with males homozygous for a defective transposon, expressing the transposase. The F1 male progeny were crossed with virgin w1118 females. The F2 Male progeny that had coloured eyes and lacked the transposon's genetic markers were selected, as they contain a new stable insertion on an autosomal chromosome. These males were crossed with flies heterozygous for GMR-GAL4 on chromosome 2, balanced by CyO chromosome, and homozygous for UAS-127Q on chromosome 3. The resulting F3 progeny were screened for eye phenotype. Once a modifier was found, a single male was crossed to female (CyO;TM3)/Xa. The resulting male progeny were crossed to w1118 flies to separate the P-elements. This resulted in colored-eye progeny that carry a balancer for one chromosome and a Pelement on another. Males from such progeny were tested for modifier activity by crossing to female w;GMR/CyO;127Q/127Q. The lines were established by crossing the latter males to (CyO;TM3)/Xa, and by crossing the resulting flies carrying CyO and TM3 balancers. EP55: source of transposable P-element;  $P[\Delta 2-3]$ : source of transposase; F: female; M: male; CyO: balancer chromosome 2; TM3: balancer chromosome 3. Xa: translocation (2;3) Xa. (Chromosome 4 is omitted.)











#### FIGURE 9A

dTPR2 Protein 508 amino acids

MDDEVIEISDSEREETSSNSEMDVEITTEQPTIDVKAEQIVPKDAATIAEEKKKLG NDQYKAQNYQNALKLYTDAISLCPDSAAYYGNRAACYMMLLNYNSALTDARH AIRIDPGFEKAYVRVAKCCLALGDIIGTEQAVKMVNELNSLSTAVAAEQTAAQK LRQLEATIQANYDTKSYRNVVFYLDSALKLAPACLKYRLLKAECLAFLGRCDEA LDIAVSVMKLDTTSADAIYVRGLCLYYTDNLDKGILHFERALTLDPDHYKSKQM RSKCKQLKEMKENGNMLFKSGRYREAHVIYTDALKIDEHNKDINSKLLYNRALV NTRIGNLREAVADCNRVLELNSQYLKALLLRARCYNDLEKFEESVADYETALQL EKTPEIKRMLREAKFALKKSKRKDYYKILGIGRNASDDEIKKAYRKKALVHHPD RHANSSAEERKEEELKFKEVGEAYAILSDAHKKSRYDSGQDIEEQEQADFDPNQ MFRTFFQFNGGGRNNSSFNFEF

#### FIGURE 9B

dTPR2 cDNA 2239 base pairs

GGCACGAGCCACTACTTCGCATGGCACGCTTTTTTCCGTGTGCTCGGTTCGTT CGGCCATACAAAACACAAAATTCAAGTTTAAAAACTAAATAGGCAACTAAAA GGGAAGCCGCAGCGAATAAAGTGATTTGCTGAAAGAGACGTAAGAAAGTTA ATCGCATCGAAGGCACCAGAAATCGGGGATTTCTAACACGGCGCGCGTGCGA CGTACATACATACGCAAGCGCACACACACACGAACAATTACTTGCCATTGAC GCAAAAGCGAAAAAGCAGTGGAATAAAGGGGAATTGACAAATAACAACGTT TTGCAAGCACTGGACTCTGGTCGCTGGTGTTCTTTCATTTTGTAATTGCCACG CATGGACGACGAAGTAATTGAAATTAGCGACAGCGAACGCGAAGAAACCTC ATCGAACTCCGAAATGGATGTGGAAATAACGACAGAACAGCCAACCATCGAT GTCAAAGCAGAGCAAATTGTGCCCAAGGACGCGGCAACCATTGCCGAGGAG AAGAAGAACTGGGCAACGACCAATACAAGGCGCAGAACTATCAGAATGCA CTCAAGCTCTACACGGATGCCATATCGCTGTGTCCGGACTCGGCGGCATACTA TGGCAATCGGGCCGCCTGCTACATGATGCTGCTCAACTATAATAGCGCCCTG ACCGACGCCGACACGCCATACGCATCGATCCGGGCTTCGAGAAGGCCTACG TCCGTGTGGCCAAGTGCTGTCTGGCCCTGGGCGACATTATTGGCACCGAACA GGCCGTCAAAATGGTCAACGAGCTGAATTCGCTTAGCACGGCTGTTGCTGCC GAACAGACGGCGCCAAAAGTTGCGCCAATTGGAGGCCACCATTCAGGCG AACTACGATACGAAATCCTATCGCAATGTGGTCTTCTATTTGGATAGTGCCTT GAAATTGGCGCCCGCCTGTTTGAAATATCGTCTACTCAAGGCTGAGTGCCTTG CATTTTTGGGGCGATGTGATGAGGCCTTGGACATTGCGGTCAGTGTAATGAA ACTGGATACCACATCGGCGGATGCGATATACGTGAGAGGTCTGTGCCTGTAC TACACGGACAACCTGGACAAGGGAATTCTTCATTTCGAGCGCGCCCTGACCC TCGACCCGGACCACTACAAGTCCAAGCAGATGCGCAGCAAATGCAAGCAGCT CAAGGAGATGAAGGAGAACGGCAATATGCTATTCAAGTCGGGTCGGTATCGC GAGGCACACGTTATCTACACGGACGCCCTGAAGATCGATGAACACAACAAGG ATATCAATTCGAAATTGCTTTACAATCGGGCTTTGGTCAACACGCGTATTGGC AATTTGCGAGAGGCCGTGGCCGATTGCAATCGAGTGCTGGAGCTGAATAGTC AGTATCTGAAGGCTCTGTTGCTGCGAGCGCGCTGCTACAATGATCTGGAGAA GTTCGAGGAGTCGGTGGCGGACTATGAGACGGCGCTGCAGCTGGAGAAGAC GCCGGAGATTAAGCGAATGCTGCGCGAGGCCAAGTTTGCGTTGAAGAAGTCG AAGCGAAAGGACTACTACAAGATCCTGGGCATTGGACGCAATGCGTCCGACG ACGAGATCAAGAAGGCGTATCGCAAAAAGGCGCTGGTACATCATCCGGATCG

#### FIGURE 10A

dMLF Protein 273 amino acids
MSLFGALMGDFDDDLGLMNNHMNHTMNAMNMQMRSMNRLMNSFMPDPFMQ
VSPFDQGFQQNALMERPQMPAMPAMGLFGMPMMPNFNRLLNADIGGNSGASF
CQSTVMTMSSGPDGRPQIYQASTSTKTGPGGVRETRRTVQDSRTGVKKMAIGHH
IGERAHIIEKEQDMRSGQLEERQEFINLEEGEAEQFDREFTSRASRGAVQSRHHAG
GMQAIMPARPAAHTSTLTIEPVEDDDDDDDDDCVIQEQQPVRSSAGRHYSSAPTAP
ONRYNY

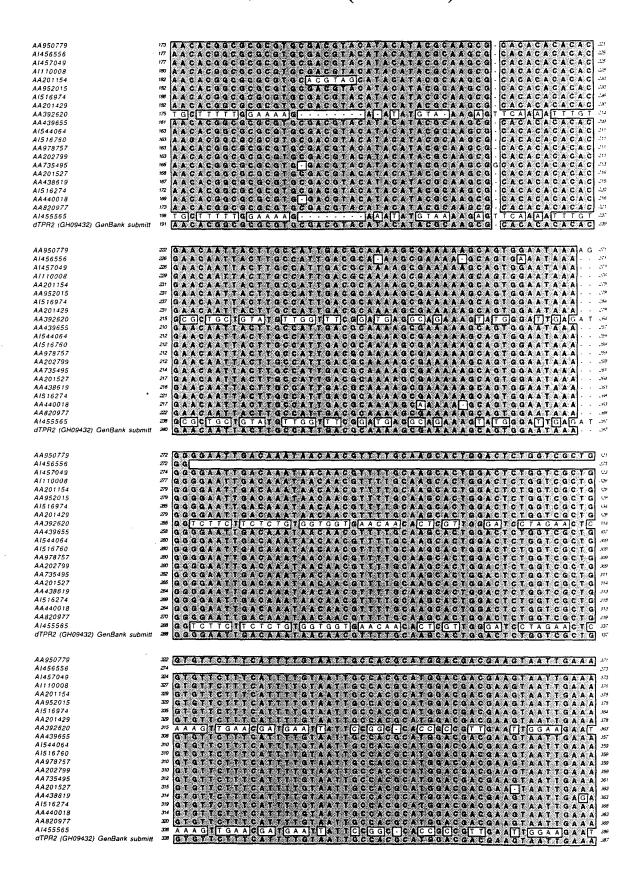
#### FIGURE 10B

dMLF cDNA 1753 base pairs GGCACGAGGAAAATATTCGTGAAAATTCTGCATACGGAAAGAAGAAAATTC GAGCAACAGAAAGCCAACACAATCCACAAAAATGTCTTTATTCGGAGCGTTG ATGGGTGATTTCGACGACGATCTCGGCCTTATGAACAACCACATGAACCACA CTATGAACGCGATGAACATGCAGATGCGCTCGATGAATCGCCTGATGAACAG CTTTATGCCCGATCCCTTCATGCAGGTCTCGCCCTTTGACCAGGGATTCCAGC CTTCGGCATGCCCATGATGCCAAACTTTAATCGCCTGTTGAACGCTGATATTG GTGGCAATTCAGGCGCATCCTTCTGCCAGAGCACCGTGATGACCATGTCATC GGGTCCCGATGGGCGTCCTCAGATCTACCAGGCCAGCACTAGTACCAAAACA GGACCGGGAGGCGTTCGTGAGACCCGCAGGACGGTGCAGGACTCGCGCACT GGGGTGAAGAAGATGGCCATTGGTCATCACATCGGCGAGCGGGCACACATTA TTGAGAAAGAGCAGGACATGCGCTCAGGACAACTGGAGGAGCGCCAGGAGT TCATTAATCTGGAGGAGGAGAAGCCGAGCAGTTTGACAGGGAGTTTACATC GCGCGCTAGTCGCGGAGCGGTGCAGTCAAGACATCATGCTGGTGGCATGCAG GCCATCATGCCCGCCCGTCCAGCGGCACACACCTCGACGTTGACCATTGAGC CAGTGGAGGACGACGACGATGATGATGACTGTGTAATCCAGGAGCAGC AACCGGTTCGCTCCGCGGGCCGCCATTATTCCAGTGCGCCAACGGCACC GCAGAACAGATATAATTACTAAATCTAAAGTCAATACAGTATATTTTACTAA CTATCCGATAAAACAGAACAGAATTGCATACTATAAATTTCTGCTAATTAC ACAGAGCAGCATACATCCACATCCCTATGCCGCCAATCCGAGGCGCCAACAA CGTGCCGTAAAACATTTTCACACGGAGGACGAAGCGGCCAGCTCCTACAAGG CGGTCAAGCGCGGCAAGAAGAAGTAGTAGAAACGTGATCATCTGTATGCCAA CATCTTCCGCATCGCACACTCAAAAACACTAGGAAGCAAAGCGTTGGGTTCT CCAGTTCTGTCTTATCCTGCGTGAGTCGACCAGAATGCAACACTAAAAAATGT ACAACTTCAAGATGCTATTGATGTGCACGCAGGATACAGAACAACTTGCTTA AATTTACTTAAAACAAATGTGACTATTCAACGCCGAAATCATTACAACACAC TCGTAATTATAAGTTTGAATTATTTGATTAATTCTCAAGTTTTTAGATTTTGTT AGCCACTAAGCTTTAAATTATGGATGCCAGTTAGCGTGCAAATGAACACAAT TGATTTGAAGGCTCCGAACGATAGAAAACAACAATTACCAATTCCCCAAATA ATTACATTATAATAGTAAAAAAAAAAAAAAAAAAA

### FIGURE 11A

### ClustalW Formatted Alignments

AA950779	GCATGGCACGCTTTTTCCGTGCTCGGTTC
A1456556	CTTCGCATGAGAGAGAGAGTTTTTCGATAGGAGTTCG-
A1457049	' CTTCGC AT G GCACGCTTTTTTCCGTGTGCTCGGTTC  *
Al11000B	CTACTTCGCATGGCACGCTTTTTTCCGTGTGCTCGGTTC
AA201154	
AA952015	CACTACTTCGCATGGCACGCTTTTTTCCGTGTGCTCGGTTC
AI516974	' T T C C A C C A C T A C T T C G C A T G G C A C G C T T T T T T C C G T G T G C T C G G T T C C G
AA201429	AACTACTTCGCATGCCCCCTTTTTTCCGTGTGCCCGGTTC]
AA392620	TITAACACAAATCITCC-CATGAITTTATTA
AA439655	TITTOCATA CACACITICA
A1544064	
A1516760	CITITIC QT AT ACT C AGT TC 2
AA978757	CTTTTTCCGTGTGCTCGGTTC
AA202799	' CTITITICG STGT SCT C G STTC =
AA735495	/ ACCETTITITE CATACTEC TO STORE
AA201527	
	GCACGCTTTTTTCCGTGTGCTCGGTTC
AA438619	
AI516274	CATGOCACGCTTTTTCCGTGTGCTCGGTTC//
AA440018	' GCACGCTTTTTTCCGTGTGCTCGGTTC
AA820977	GCATGGCACGCTTTTTTCCGTGTGCTCGGTTC
A1455565	' A TA T G TA TA T T T C T G T T TA T T T T A CA CA CA A A T C T C C - C A T G A T T T A T T T A T
dTPR2 (GH09432) GenBank submitt	
UTFA2 (GRU9432) GENBANK SUDMILL	' G G C A C G A G C C A C T A C T T C G C A T G G C A C G C T T T T T T C C G T G T G C T C G G T T C T V
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A1110008	
AA201154	
	The standard of the standard o
AA952015	GTTCGGCCATACAAACA CAAAATTCAA GTTTAAAAACTAAATAGG
AI516974	- 4 GITCGGCCATACAAACA CAAAATTCAA GTTTAAAAACTAAATGGG 🗥
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AA201527	# GTTGGGGGATAGAAAAGA - GAAAATTGAA GTTTAAAAAGTAAATAGG
AA438619	The state of the s
AI516274	PGTTCGGGCATACAAAACA CAAAATTCAA GTTTAAAAAACTAAATAGG
AA440018	BIGIT COGCCATACAAAA CA CAAAATT CAA - GT TAAAAA CTAAATA G G
AA820977	" GTTCGGCCATACAAAACA CAAAATTCAA GTTTAAAAACTAAATAGG -
A1455565	- ATGTTGCCGAAAAAAATCCAAGAAAGAACATTTAAAAATGTGAACTT
dTPR2 (GH09432) GenBank submitt	5 GTTGGGCCTTACAAACA CAAAATTCAA GTTTAAAAACTAAATAGG .
dTPH2 (GH09432) GenBank submitt	
	51 GIT CGGCCI AGAAAACA CAAAATICAA GITTIAAAAACTAAATAGG **
AA950779	
	STEGET COGCERTAGRARACA CARRATTCAR GTTTARRACTARATAGG
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AA950779 AI456556 AI457049 AI110008 AA201154 AA952015 AI516974 AA201429 AA392620 AA499655 AI544064 AI516760 AA978757	51 GTTGGGCGATAGAAAGA - CAAAATTCAA - GTTTTAAAAACTAAATAGG **  52 GAACTAAAAGGGAAGCCGCAGC - GA - ATAAAGTGATTTGCTGAAAG - GCAACTAAAAAGGGAAGCCGCAGC - GA - ATAAAGTGATTTGCTGAAAG - GCAACTAAAAAGGGAAGCCGCAGC - GA - ATAAAGTGATTTGCTGAAAG - GCAACTAAAAGGGAAGCCGCAGC - GA - ATAAAGTGATTTGCTGAAAG - GCAACTAAAAGGGAAGCGCGCAGC - GA - ATAAAGTGATTTTCCTGAAAG - GCAACTAAAAGGGAAGCCGCAGC - GA - ATAAAGTGATTTTCCTGAAAGGG- CAACTAAAAGGGAAGCCGCAGC - GA - ATAAAGTGATTTTCCTGAAAGGG- CAACTAAAAGGGAAGCCGCAAGC - GA - ATAAAGTGATTTTCCTGAAAGGG- CAACTAAAAGGGAAGCCGCAAGC - GA - ATAAAGTGATTTTCCTGAAAGGG- CAACTAAAAGGGAAGCCGCAAGC - GA - ATAAAGTGATTTTCCTGAAAGGG- CAACTAAAAGGGAAGCCCCCAAGC - GA - ATAAAAGTGATTTTCCTGAAAGGG- CAACTAAAAGGGAAGCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTGAAAGGG- CAACTAAAAGGGAAGCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTGAAAGGG- CAACTAAAAAGGGAAGCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTGAAAGGG- CAACTAAAAGGGAAGCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAGGGC- CAACTAAAAGGGAAGCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAGGGCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAGGGCCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAGGGCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAGGGCCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAGGGCCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAGGGCCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAAGGGCCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAAGGCCCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAAGGGCCCCCCCAAGCC - GA - ATAAAAGTGATTTTCCTTCAAAGGGCCCCCCCAAGCC - GA - ATAAAAAGTGATTTTCCTTCAAAAGGCCCCCCCAAGCC - GA - ATAAAAA
AA950779 AI456556 AI457049 AI110008 AA201154 AA952015 AI516974 AA201429 AA392620 AA439655 AI544064 AI516760	51 GTTGGGCGATAGAAAGA - CAAAATTCAA - GTTTTAAAAACTAAATAGG **  52 GAACTAAAAGGGAAGCCGCAGC - GA - ATAAAGTGATTTGCTGAAAG - GCAACTAAAAAGGGAAGCCGCAGC - GA - ATAAAGTGATTTGCTGAAAG - GCAACTAAAAAGGGAAGCCGCAGC - GA - ATAAAGTGATTTGCTGAAAG - GCAACTAAAAGGGAAGCCGCAGC - GA - ATAAAGTGATTTGCTGAAAG - GCAACTAAAAGGGAAGCGCGCAGC - GA - ATAAAGTGATTTTCCTGAAAG - GCAACTAAAAGGGAAGCCGCAGC - GA - ATAAAGTGATTTTCCTGAAAGGG- CAACTAAAAGGGAAGCCGCAGC - GA - ATAAAGTGATTTTCCTGAAAGGG- CAACTAAAAGGGAAGCCGCAAGC - GA - ATAAAGTGATTTTCCTGAAAGGG- CAACTAAAAGGGAAGCCGCAAGC - GA - ATAAAGTGATTTTCCTGAAAGGG- CAACTAAAAGGGAAGCCGCAAGC - GA - ATAAAGTGATTTTCCTGAAAGGG- CAACTAAAAGGGAAGCCCCCAAGC - GA - ATAAAAGTGATTTTCCTGAAAGGG- CAACTAAAAGGGAAGCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTGAAAGGG- CAACTAAAAGGGAAGCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTGAAAGGG- CAACTAAAAAGGGAAGCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTGAAAGGG- CAACTAAAAGGGAAGCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAGGGC- CAACTAAAAGGGAAGCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAGGGCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAGGGCCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAGGGCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAGGGCCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAGGGCCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAGGGCCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAAGGGCCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAAGGCCCCCCCCAAGC - GA - ATAAAAGTGATTTTCCTTCAAAAGGGCCCCCCCAAGCC - GA - ATAAAAGTGATTTTCCTTCAAAGGGCCCCCCCAAGCC - GA - ATAAAAAGTGATTTTCCTTCAAAAGGCCCCCCCAAGCC - GA - ATAAAAA
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AA950779 AI456556 AI457049 AI110008 AA201154 AA952015 AI516974 AA201429 AA392620 AA499655 AI544064 AI516760 AA978757 AA202799 AA 735495 AA201527	57 G A A C T A A A A G G G A A G C C G C A G C
AA950779 AI456556 AI457049 AI110008 AA201154 AA952015 AI5166974 AA201429 AA392620 AA439655 AI516760 AA978757 AA202799 AA 735495 AA201527 AA438619	51 GTTCGGCGATACAAAGA - CAAAATTCAA GTTTTAAAAACTAAATAGG 6  52 CAACTAAAAGGGAAGCCGCAGC - GA ATAAAGTGATTTGCTGAAAG 6  53 CAACTAAAAAGGGAAGCCGCAGC - GA ATAAAGTGATTTGCTGAAAG 6  54 CAACTAAAAAGGGAAGCCGCAGC - GA ATAAAGTGATTTGCTGAAAG 6  55 CAACTAAAAAGGGAAGCCGCAGC - GA ATAAAGTGATTTGCTGAAAG 6  56 CAACTAAAAAGGGAAGCCGCAGC - GA ATAAAGTGATTTTGCTGAAAG 6  57 CAACTAAAAAGGGAAGCCGCAGC - GA ATAAAGTGATTTTGCTGAAAG 6  58 CAACTAAAAAGGGAAGCCGCAGC - GA ATAAAGTGATTTTGCTGAAAG 6  59 CAACTAAAAAGGGAAGCCGCAGC - GA ATAAAGTGATTTTGCTGAAAG 6  50 CAACTAAAAAGGGAAGCCGCAGC - GA ATAAAGTGATTTTGCTGAAAG 6  50 CAACTAAAAGGGAAGCCGCAGC - GA ATAAAGTGATTTTTTTTTTTCAAAATTA 6  50 CAACTAAAAGGGAAGCCGCAGC - GA ATAAAGTGATTTTTTTTTTTTTTTTTTTTTTTTT
AA950779 AI456556 AI457049 AI110008 AA201154 AA952015 AI516974 AA201429 AA392620 AA439655 AI54064 AI516760 AA978757 AA202799 AA735495 AA201527 AA438619 AI516274	51 GTTGGGCGATAGAAAGA CAAAATICAA - GTTTAAAAACTAAATAGG **  52 CAACTAAAAGGGAAGCCGCAGC
AA950779 AI456556 AI457049 AI110008 AA201154 AA952015 AI516974 AA201429 AA392620 AA499655 AI516760 AA978757 AA202799 AA735495 AA201527 AA438619 AI516274 AA440018	57 G A A C T A A A A G G G A A G C G C A G C
AA950779 AI456556 AI457049 AI110008 AA201154 AA952015 AI516974 AA201429 AA392620 AA439655 AI544064 AI516760 AA978757 AA202799 AA735495 AA201527 AA438619 AI516274 AA440018 AA820977	51 GTTCGGCGATAGAAAGA
AA950779 AI456556 AI457049 AI110008 AA201154 AA952015 AI516974 AA201429 AA392620 AA439655 AI544064 AI516760 AA978757 AA202799 AA735495 AA201527 AA438619 AI516274 AA440018 AA820977 AI455565	57 GAACTAAAAGGAAAGCA
AA950779 AI456556 AI457049 AI110008 AA201154 AA952015 AI516974 AA201429 AA392620 AA439655 AI544064 AI516760 AA978757 AA202799 AA735495 AA201527 AA438619 AI516274 AA440018 AA820977	57 GAACTAAAAGGAAAGCA
AA950779 AI456556 AI457049 AI110008 AA201154 AA952015 AI516974 AA201429 AA392620 AA439655 AI544064 AI516760 AA978757 AA202799 AA735495 AA201527 AA438619 AI516274 AA440018 AA820977 AI455565	57 G A A C T A A A A G G A A G C G C A G C
AA950779 AI456556 AI457049 AI110008 AA201154 AA952015 AI516974 AA201429 AA392620 AA439655 AI544064 AI516760 AA978757 AA202799 AA735495 AA201527 AA438619 AI516274 AA440018 AA820977 AI455565	57 GAACTAAAAGGAAAGCA
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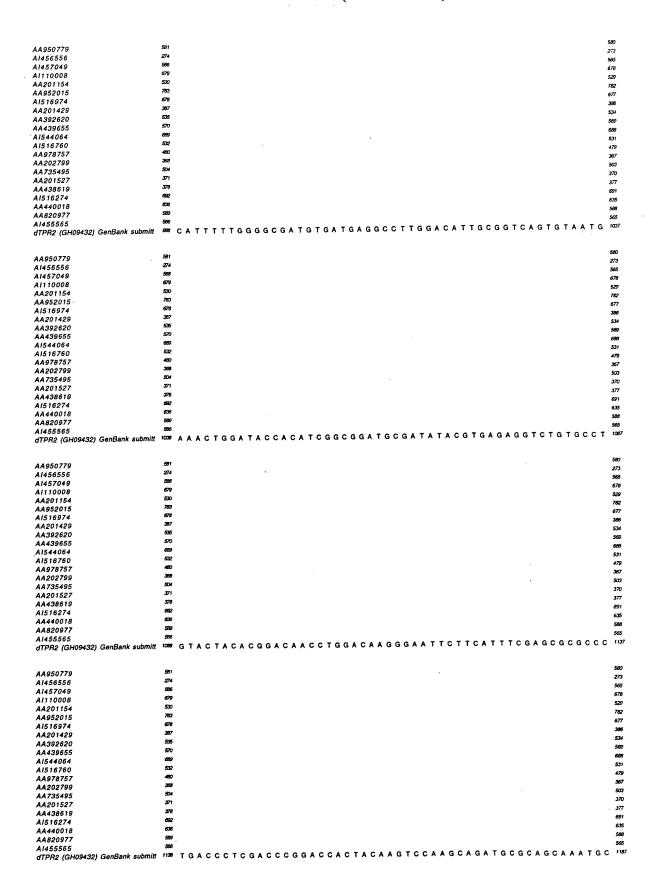


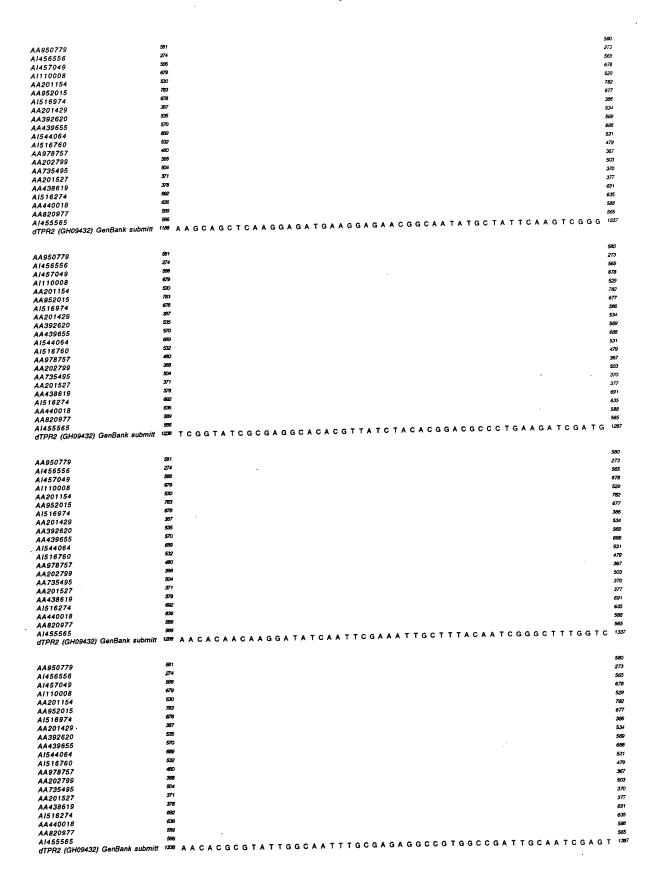
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AI456556 AI457049 AI110008 AA201154 AA952015 AI516974 AA201429 AA392620 AA439655 AI544064 AI516780 AA978757 AA202799 AA735495 AA201527 AA438619 AI516274 AA440018 AA820977	GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATTGCCGAGAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATTGCCGAGAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATTGCCGAGAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATTGCCGAGAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAAAAA
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A1456556 A1457049 A1110008 AA201154 AA952015 A1516974 AA201429 AA392620 AA439655 A1544064 A1516760 AA978757 AA202799 AA735495 AA201527 AA438619 A1516274 A440018 AA820977 A1455565	GCCCAAGGACGCGCAACCATIGCCGAGGAGAAGAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAAAA
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A1456556 A1457049 A1110008 A201154 AA952015 A1516974 AA201429 AA392620 AA439655 A1544064 A1516760 AA978757 AA202799 AA735495 AA201527 AA438619 A1516274 AA440018 AA820977 A1455565 dTPR2 (GH09432) GenBank submitt	GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAAACTGGGCAACG GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAACTGGGCAACG GCCCAAGGACGCGCAACCATTGCGGAAGAAAAAACTGGGCAACG GCCCAAGGACGCGCAACCATTGCGGAAGAAAAAACTGGGCAACG GCCCAAGGACGCGCAACCATTGCGGAAGAAAAAACTGGGCAACG GCCCAAGGACGCGCAACCATTGCGGAAGAAAAAACTGGGCAACG GCCCAAGGACGCGCAACCATTGCGAGAAAAAAACTGGGCAACG GCCCAAGGACGCGCAACCATTGCGAGAAAAAAACTGGGCAACG GCCCAAGGACGCGCAACCATTGCGAGAAAAAAACTGGGCAACG GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAACTGGGCAACG GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAACTGGGCAACG GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAACTGGGCAACG GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAACTGGGCAACG GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAACTGGGCAACG GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAACTGGGCAACG GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAAACTGGGCAACG GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAAACTGGGCAACG GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAAACTGGGCAACG GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAAACTGGGCAACGG GCCCAAGGACGCGCAACCATTGCCGAGGAAAAAAAACTGGGCAACGG GCCCAAGGACGCCAACCATTGCCGAGGAAAAAAAACTGGGCAACGG GCCCAAGGACGCCAACCATTGCCGAGGAAAAAAAACTGGGCAACGG GCCCAAGGACGCAACCATTGCCGAGGAAAAAAACTGGGCAACGG GCCCAAGGACGCAACCATTGCCGAGGAAAAAAAACTGGGCAACGG GCCCAAGGACGCCAACCATTGCCGAGGAAAAAAACTGGGCAACGG
AI456556 AI457049 AI110008 AA201154 AA952015 AI516974 AA201429 AA392620 AA4396655 AI544064 AI516780 AA978757 AA202799 AA735495 AA201527 AA438619 AI516274 AA440018 AA820977 AI455565 dTPR2 (GH09432) GenBank submitt	GCCCAAGGACGCGCAACCATIGCCGAGGAGAAGAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAAAA
AI456556 AI457049 AI110008 AA201154 AA952015 AI516974 AA201429 AA392620 A4439655 AI544064 AI516780 AA978757 AA202799 AA735495 AA201527 AA438619 AI516274 AA440018 AA820977 AI455565 dTPR2 (GH09432) GenBank submitt AA950779 AI456556 AI457049 AI150008	GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAGGAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAAGAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAAGAAAAAAAAAAACTGGGCAACG  GCCCAAGGACGCGCAACCATIGCCGAAGAAAAAAAAAAAA
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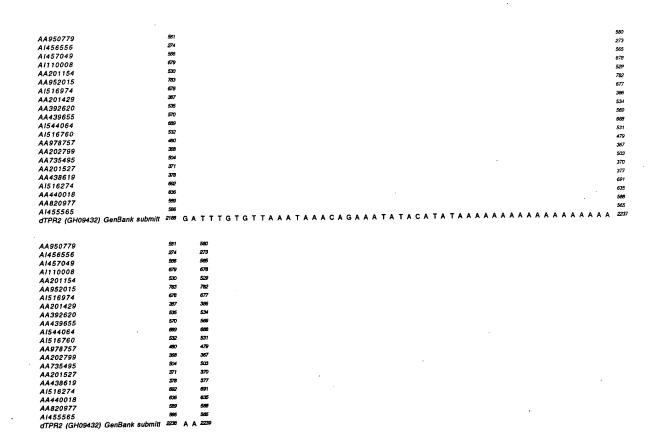


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AA439655	570																							6	98
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AA438619	378																								91
AI516274	692																								35
AA440018	636																								88
AA820977	589																								65
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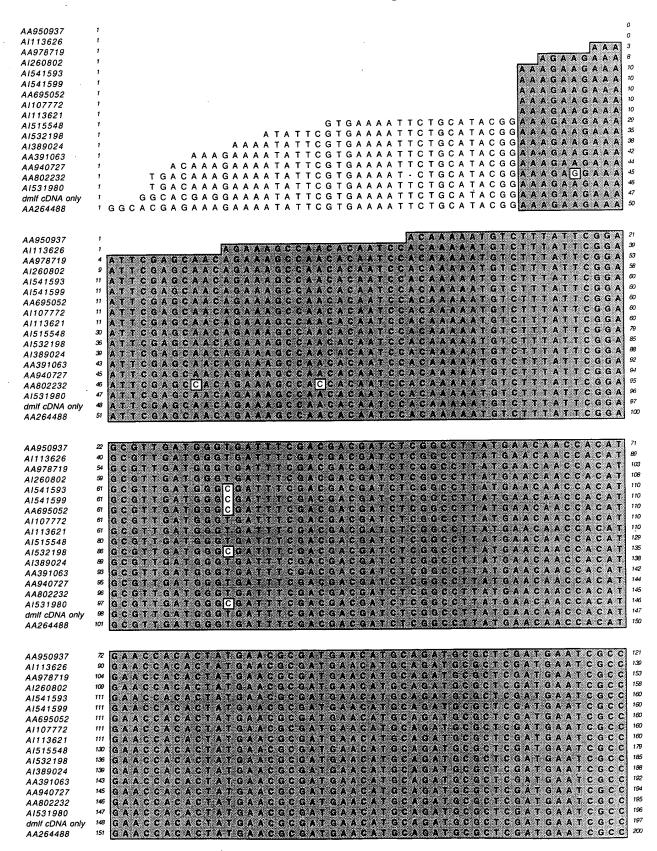
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	AA391402 AI514849 AI519786 AI546378 AA438290 AA820520 AA941597 AI455870 AA950277 AA941028 AA951077 AA951083 AA949900 AA541065 AA441093 dTPR2 (GH09432) GenBank submitt AI456052 AA391402 AI514849	664 632 542 561 618 583 551 547 488 247 171 512 700 597 1641		c G	c	ΤG	G.	ТА	C /	λT	C A	. т (	сс	G G	ΑΊ	г <b>С</b> (	A E	C /	A C	: G	C /	Α Α	Α	C /	А G	С	A G	т	G (	c c	G	A G	S G	А	3 C I	G	553 553 553 553 553 553 553 553 554 554
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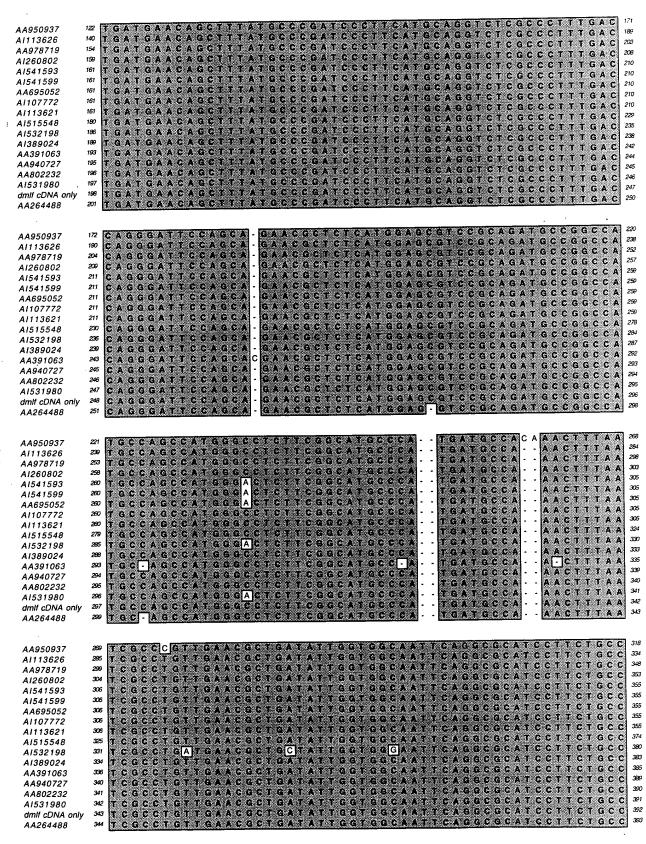
·																											
A1456052	590																										581
AA391402	654																										65.7
AI514849	632																										651
AI519786	562																										561
A1546378	542																										541
	561																										(35)
AA438290	618																										(1)
AA820520																											580
AA941597	583																										550
A1455870	551																										54
AA950277	547																										49,1
AA941028	488																										244
AA951077	247																										170
AA951083	171																										511
AA949900	512																										666
AA541065	700																										506
AA441093	597																						_				
dTPR2 (GH09432) GenBank submitt	1741	TGT	T C G	GA	ΤG	СТ	CA	CA	A G	AAG	G T (	GC	GC	ΤA	CG	A C	A G	C	G G	СС	A G	i G	А Т	АТ	CC	3 A G	1750
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A1456052	590																										500
AA391402	654																										$65^{\circ}$
A1514849	632																										631
	562																										561
A1519786	542																										541
A1546378	561																										571
AA438290																											617
AA820520	618 583																										592
AA941597																											550
A1455870	551																										54
AA950277	547																										4.0
AA941028	488																										24
AA951077	247																										170
AA951083	171																										51:
AA949900	512																										690
AA541065	700																										596
AA441093	597											•						_									
dTPR2 (GH09432) GenBank submitt	1791	GAC	G C A	GG	AG	CA	A G	СС	G A	СТ	TC	3 A 1	CC	GA	AT	CA	. A A	A T	G T	тс	C	a C	A C	Α	1 1	СТТ	1840
277 / L (27700 10-)																											
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A1456052	590																										580
A1456052	590 654																										653
AA391402	654																										653 631
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AA391402 AI514849 AI519786	654 632 562																										653 631
AA391402 A1514849 A1519786 A1546378	654 632 562 542																										653 631 561
AA391402 AI514849 AI519786 AI546378 AA438290	654 632 562 542 561																										653 631 561 541
AA391402 AI514849 AI519786 AI546378 AA438290 AA820520	654 632 562 542 561 618																										653 631 561 541 560
AA391402 AI514849 AI519786 AI546378 AA438290 AA820520 AA941597	654 632 562 542 561 618																·.										653 631 561 541 560 61
AA391402 AI514849 AI519786 AI546378 AA438290 AA820520 AA941597 AI455870	654 632 562 542 561 618 583 551																										653 631 561 541 560 617 580
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AA391402 AI514849 AI519786 AI546378 AA438290 AA820520 AA941597 AI455870 AA950277 AA941028 AA951077 AA951077 AA951083 AA949900 AA541065 AA441093 dTPR2 (GH09432) GenBank submit	654 632 562 542 561 618 583 551 547 488 247 171 512 700 597 † 1841	· cc.	А А <sup>-</sup>	ттс		CG	GC	G G	. Т G	GC	C G	G A /	<b>ч</b> т /	4 A 1	τ τ ο	T A C	r c (	GΤ	тс	ΑĀ	С.	ΥТ	ТО	6 A :	GТ	тс 1	653 631 561 561 560 617 560 560 548 246 170 511 639 560
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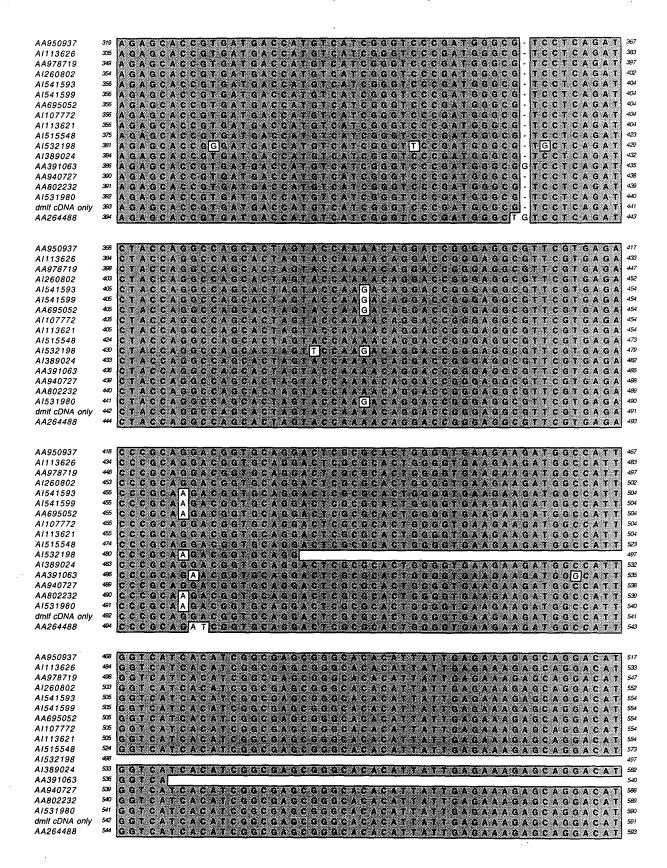
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A1455870	551		546
AA950277	547		487
AA941028	488		246
AA951077	247		170
AA951083	171		511
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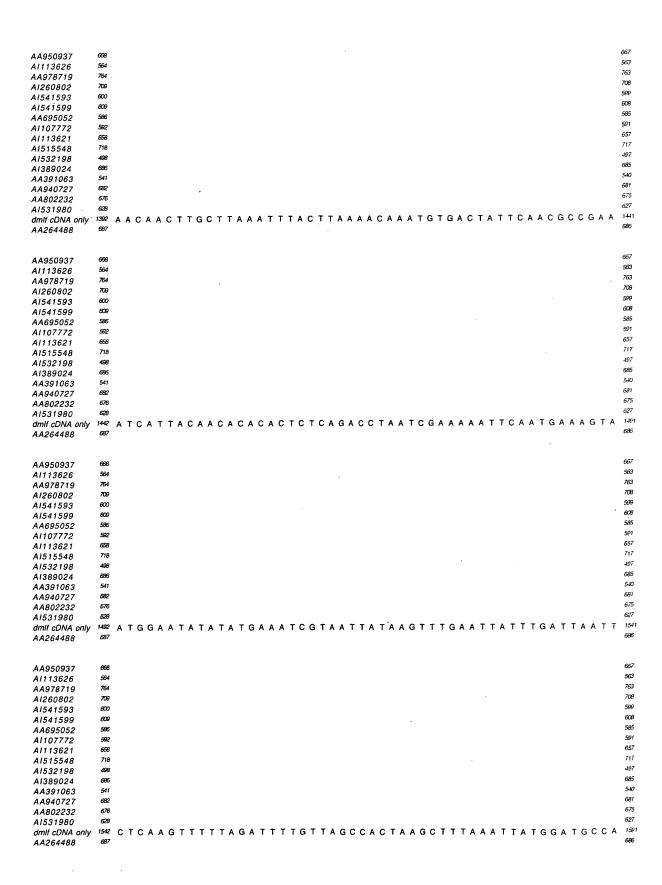


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AI113626 AA978719 AI260802 AI541593 AI541599 AA695052 AI107772 AI113621 AI515548 AI532198 AI389024 AA391063 AA940727 AA802232 AI531980 dmlf cDNA only AA264488	564 764 709 600 609 586 582 658 718 498 686 541 682 687 687		Τ.	<b>A</b> T	ГА	. А	т	т/	A C		Α.	A A	т	С 1	ГА	Α ,	A G	тс	; A	ΑΊ	- A	С.	A G	ìΤ	A	T A	Т	т -		A	C 1	ΓΑ	A	С	ΤA	ιт	С	C G	563 763 708 599 606 585 591 497 497 685 540 681 675 627 941 686
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A1113626 AA978719 A1260802 A1541593 A1541599 AA695052 A1107772 A1113621 A1515548 A1532198 A1532198 A1389024 AA391063 AA940727 AA802232 A1531980 dmlf cDNA only AA264488 AA950937 A1113626 AA978719	564 764 709 600 609 586 582 688 686 541 686 687 687 687 688 564 764		т.	<b>A</b> 1	ГА	. A	т	т,	A C	. т	Α.	Α Α	. т	C 1	ГА	Α Α	₹ G	тс	; A	ΑΊ	- А	С.	A G	ìТ	Α ΄	ТА	Т	т.		A	C 1	ГА	Α	С	ТА	νт	С	C G	563 763 708 599 608 551 657 717 497 685 5-40 687 941 686 667 563 763 763 763 763
A1113626 AA978719 A1260802 A1541593 A1541599 AA695052 A1107772 A1113621 A1515548 A1532198 A1389024 AA391063 AA940727 AA802232 A1531980 dmlf cDNA only AA264488 AA950937 A1113626 AA978719 A1260802	564 764 709 600 596 592 583 584 686 541 682 687 682 687 683 684 764 764 704		т.	A T	г А	. А	т	т,	A C	. т	Α.	Α Α	. т	C 1	ГА	Α /	A G	тс	; A	АΊ	- A	С.	A G	ìТ	Α ΄	T A	T	т -		A	C 1	ГА	Α	С	ТА	νТ	С	CG	563 763 708 599 608 585 591 657 717 497 685 540 687 697 941 686 667 563 763 763 763 763 768 599 608
AI113626 AA978719 AI260802 AI541593 AI541599 AA695052 AI107772 AI113621 AI515548 AI532198 AI389024 AA391063 AA940727 AA802232 AI531980 dmlf cDNA only AA264488 AA950937 AI113626 AA978719 AI260802 AI541593	564 764 709 600 600 566 562 568 541 662 676 623 627 687 687 687 687 687 687 687 687 687 68		Τ.	Α 7	г А	. А	т	т,	A C	. т	Α.	Α Α	т	<b>C</b> 1	ГА	Α /	¼ G	тс	: А	ΑΊ	- A	С.	A G	ìТ	Α .	T A	т	т -	. т	Α	Cl	ГА	Α	С	ТА	ΥТ	С	CG	563 763 708 509 608 555 551 657 717 497 665 540 681 675 627 941 686 667 763 763 763 768 559 608
AI113626 AA978719 AI260802 AI541593 AI541599 AA695052 AI107772 AI113621 AI515548 AI532198 AI389024 AA391063 AA940727 AA802232 AI531980 dmlf cDNA only AA264488 AA950937 AI113626 AA978719 AI260802 AI541593 AI541599	564 764 709 600 609 586 658 718 498 666 541 667 676 677 687 769 769 663 564 779 663 664 665 667 764 769 666 666 667 769 666 667 667 667 667		т.	Α 7	Г А	. А	т	т,	A C	. т	Α.	Α Α	т	<b>C</b> 1	ГА	Α ,	A G	тс	; A	АТ	- A	С.	A G	ìТ	Α ΄	TA	т	т .	. т	Α	Cl	ГА	Α	С	ТА	νТ	С	CG	563 768 768 569 569 565 591 657 717 665 540 681 675 540 681 675 540 686 686 687 941 686 687 696 696 696 697 698 698 698 698 698 698 698 698 698 698
A1113626 AA978719 A1260802 A1541593 A1541599 AA695052 A1107772 A1113621 A1515548 A1532198 A1389024 AA391063 AA940727 AA802232 A1531980 dmlf cDNA only AA264488 AA950937 A1113626 AA978719 A1260802 A1541593 A1541599 AA695052	564 764 709 600 609 596 596 596 597 686 686 686 687 682 687 764 764 764 764 764 764 764 764 764 76		т.	<b>A</b> 7	Г А	. А	т	т,	A C	. т	Α.	Α Α	. т	C 1	ГА	Α Α	A G	тс	: A	АТ	- A	С.	A G	ìТ	Α	TA	Т	Т.		A	C 1	ГА	Α	С	ТА	. Т	С	CG	563 7663 7686 5896 5895 591 6857 7177 6885 540 681 675 6941 686 687 708 589 608 589 608 589 608
A1113626 AA978719 A1260802 A1541593 A1541599 AA695052 A1107772 A1113621 A1515548 A1532198 A1389024 AA391063 AA940727 AA802232 A1531980 dmlf cDNA only AA264488 AA950937 A1113626 AA978719 A1260802 A1541599 AA695052 A1107772	564 764 709 600 609 596 596 698 698 698 698 698 698 764 764 774 779 600 600 600 600 600 600 600 600 600 60		т.	Α 7		. А	т	т,	A C	. т	Α.	<b>A</b> A	т	<b>C</b> 1	ГА	Α ,	√ G	тс	: A	АТ	- A	С.	A G	ìТ	Α ΄	TA	T	T		A	Cl	ΓΑ	Α	С	ТА	νТ	С	CG	563 7663 7666 599 606 595 591 657 717 497 685 540 687 541 686 587 594 608 599 608 599 608 595 591 657 708
AI113626 AA978719 AI260802 AI541593 AI541599 AA695052 AI107772 AI113621 AI515548 AI532198 AI389024 AA391063 AA940727 AA802232 AI531980 dmil cDNA only AA264488 AA950937 AI113626 AA978719 AI695052 AI541593 AI541593 AI541593 AI641593 AI641593 AI641593 AI641593 AI641593 AI6417772 AI117772	564 764 709 600 600 600 600 600 600 600 600 600 6		т.	Α 1	Г А	. А	т	т,	A C	. т	Α.	Α Α	. т	<b>С</b> 1	ГА	Α .	A G	тс	: A	ΑΊ	- A	C	A G	ìТ	Α ΄	TA	Т	T	. т	A	CI	ГА	Α	С	ТА	νТ	С	C G	563 7663 7686 5895 5891 657 591 685 5941 686 687 647 563 768 687 563 768 585 599 608 585 591 657 717 717
AI113626 AA978719 AI260802 AI541593 AI541599 AA695052 AI107772 AI113621 AI515548 AI389024 AA391063 AA940727 AA802232 AI531980 dmlf cDNA only AA264488 AA950937 AI113626 AA978719 AI260802 AI541593 AI541593 AI541599 AA695052 AI107772 AI113621 AI113621 AI515548	564 764 769 609 596 596 592 696 696 697 697 697 697 697 697 697 697		т.	<b>A</b> 7	Г А	. А	т	т,	A C	. т	Α.	<b>A</b> A	. т	<b>C</b> 1	ГА	Α ,	\ G	тс	; A	АΊ	- A	C	A G	ìТ	Α ΄	TA	Т	T	. т	A	Cl	ГА	Α	С	ТА	νт	С	C G	563 7663 7666 599 606 595 591 607 717 685 540 667 667 768 599 608 599 608 599 608 591 657 717 717 717 717 685
AI113626 AA978719 AI260802 AI541593 AI541599 AA695052 AI107772 AI113621 AI515548 AI532198 AI389024 AA391063 AA940727 AA802232 AI531980 dmlf cDNA only AA264488 AA950937 AI113626 AA978719 AI260802 AI541599 AA695052 AI107772 AI113621 AI515548 AI532198	564 764 709 500 500 500 500 500 500 500 500 500 5		т.	<b>A</b> 7	Г А	. А	т	т,	A C	. т	Α.	Α Α	. т	C 1	ГА	Α /		тс	; A	АΊ	- A	C.	A G	ìТ	Α ΄	TA	Т	т -		A	CI	ГА	A	С	ТА	т	С	CG	563 766 766 599 606 595 591 497 685 540 667 647 646 667 540 666 599 608 589 608 589 608 581 657 717 717 717
AI113626 AA978719 AI260802 AI541593 AI541599 AA695052 AI107772 AI113621 AI515548 AI389024 AA391063 AA940727 AA802232 AI531980 dmlf cDNA only AA264488 AA950937 AI113626 AA978719 AI260802 AI541593 AI541593 AI541599 AA695052 AI107772 AI113621 AI515548 AI532198 AI389024 AA391063 AA940727	564 704 600 596 596 598 598 598 598 598 598 598 598 598 598		т.	<b>A</b> 7	Г А	. А	Т	т,	A C		Α.	Α Α	. т	C 1	ГА	Α Α	A G	тс	; А	АΊ	- A	С.	A G	ìT	Α	TA	T	т -		A	Cl	ΓΑ	Α	С	ТА	. т	С	CG	563 768 708 509 608 585 717 497 685 627 941 686 687 763 763 708 585 591 608 585 591 677 717 497 681 681
AI113626 AA978719 AI260802 AI541593 AI541599 AA695052 AI107772 AI113621 AI515548 AI532198 AI389024 AA391063 AA940727 AA802232 AI531980 dmlf cDNA only AA264488 AA950937 AI113626 AA978719 AI260802 AI541599 AA695052 AI107772 AI113621 AI515548 AI532198 AI389024 AA391063 AA940727 AA802232	564 764 709 600 596 596 596 597 498 696 697 697 697 697 697 697 697 697 697		т.	<b>A</b> 7		. A	Т	т,	A C	· ·	Α.	Α Α	. т	C 1	ГА	Α Α	A G	тс	; А	ΑΊ	- A	С.	A G	т	A	TA	т	т -		A	Cl	г <b>А</b>	Α	С	ТА	. Т	С	CG	563 768 768 569 666 559 717 497 665 627 941 675 563 768 569 569 667 753 708 589 589 589 589 677 717 497 685 540 685 541 667 667 667 667 667 667 667 667 667 66
AI113626 AA978719 AI260802 AI541593 AI541599 AA695052 AI1107772 AI113621 AI515548 AI532198 AI389024 AA391063 AA940727 AA802232 AI531980 dmlf cDNA only AA264488 AA950937 AI113626 AA978719 AI260802 AI541599 AA695052 AI107772 AI113621 AI515548 AI532198 AI389024 AA391063 AA940727 AA802232 AA802232 AI531980	564 764 769 609 586 582 583 686 682 677 682 687 764 779 600 600 600 600 600 600 600 600 600 60				•																																		563 7663 7686 599 606 595 591 697 697 697 697 698 599 608 599 608 599 608 591 657 717 717 717 685 591 667 592 668 593 693 694 695 696 697 697 698 697 698 698 699 699 699 699 699 699 699 699
AI113626 AA978719 AI260802 AI541593 AI541599 AA695052 AI107772 AI113621 AI515548 AI389024 AA391063 AA940727 AA802232 AI531980 dmil cDNA only AA264488 AA950937 AI113626 AA978719 AI260802 AI541593 AI541593 AI541593 AI541593 AI541593 AI541593 AI541593 AI541593 AI541593 AI541593 AI541593 AI552198 AI389024 AA391063 AA940727 AA802232 AI531980 dmil cDNA only	564 764 709 600 596 592 593 696 696 697 697 697 697 697 697 697 697				•																																	CG	563 766 766 599 606 595 591 657 717 497 685 540 667 563 708 599 608 599 608 591 657 717 685 590 667 675 691 675 691
AI113626 AA978719 AI260802 AI541593 AI541599 AA695052 AI1107772 AI113621 AI515548 AI532198 AI389024 AA391063 AA940727 AA802232 AI531980 dmlf cDNA only AA264488 AA950937 AI113626 AA978719 AI260802 AI541599 AA695052 AI107772 AI113621 AI515548 AI532198 AI389024 AA391063 AA940727 AA802232 AA802232 AI531980	564 764 769 609 586 582 583 686 682 677 682 687 764 779 600 600 600 600 600 600 600 600 600 60				•																																		563 7663 7686 599 606 595 591 697 697 697 697 698 599 608 599 608 599 608 591 657 717 717 717 685 591 667 592 668 593 693 694 695 696 697 697 698 697 698 698 699 699 699 699 699 699 699 699

AA950937 A1113626 AA978719 A1260802 A1541593 A1541599 AA695052 A1107772 A1113621 A1515548 A1532198 A1389024 AA391063 AA940727 AA802232 A1531980 dmlf cDNA only AA264488	668 564 764 709 600 586 592 658 718 498 686 541 682 676 628 992 687	С	Α	Α (	СТ	- G	С	G	т 1	гс	: А	A	A (	· G	: <b>A</b>	А	Α (	c	G A	A	т,	A 1		G	Α /	А Т	c	G,	A A	. А	Т	с .	А <sup>-</sup>	Т А	G	A	А	Τα	G C	: A	C	A	667 563 763 708 589 608 585 591 657 717 497 685 5-40 681 675 627 1041 696
AA950937 A1113626 AA978719 A1260802 A1541593 A1541599 AA695052 A1107772 A1113621 A1515548 A1532198 A1389024 AA391063 AA940727 AA802232 A1531980 dmlf cDNA only AA264488	668 564 764 709 600 596 658 718 498 654 666 541 682 676 628 1042 687	G	Α	G	C A	A G	С	A	т,/	A C	; A	т :	c«	A C	С	A	T (	c	сс	Т	A .	πα	G C	C	G	cc	; А	A	тс	с	G	Α	G (	G C	G	С	С	A A	A C		А	С	667 563 768 599 608 585 591 657 717 497 685 540 681 675 627 1091 686
AA950937 AI113626 AA978719 AI260802 AI541593 AI541599 AA695052 AI107772 AI113621 AI515548 AI532198 AI389024 AA391063 AA940727 AA802232 AI531980 dmlf cDNA only AA264488	668 564 764 709 600 586 592 658 718 498 686 541 682 676 628 1092 627		т	G	င	G G	Т	A	Α /	A A	ı c	Α	т -	гт	т	С	A	C A	A C	G	G	Α (	G G	i <b>A</b>	C	G A	. А	G	c«	6 G	i C	С		G C		С	С		A C	: А	A	G	667 563 763 708 599 608 585 591 657 717 497 685 540 681 675 627 1141 686
AA950937 A1113626 AA978719 A1260802 A1541593 A1541593 A4695052 A1107772 A1113621 A1515548 A1532198 A1389024 AA391063 AA940727 AA802232 A1531980 dmlf cDNA only AA264488	668 564 764 709 600 596 592 598 658 718 498 636 636 636 638 1142 687		С	G	<b>3</b> 1	r c	A	A	G (	c G	G C	G	G (	A C	Α.	G	Α,	Α (		A	G T	Τ Α		iΤ	A (	G A	. А	A	c	<b>à</b> T	· G	A	Т (	C A	т	С	Т	G 1	TΑ	х Т	G	С	667 563 763 708 599 608 585 591 657 717 497 685 540 681 675 627 11191 686

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AA950937 AI113626 AA978719 AI260802 AI541599 AA695052 AI107772 AI113621 AI515548 AI532198 AI389024 AA391063 AA940727 AA802232 AI531980 dmif cDNA only AA264488	668 564 764 709 600 609 596 592 658 718 498 696 541 682 676 628 1592 687	G	т	ГА	G,	C (	3 Т	G	С	Α /	Α #	ΛТ	G	A	Α '	C /	Α (	C A	. A	Т	т	A £	Т	т .	TG	A	Α (	s G	C	т (		G	Α	А	C G	A	т	A	G /	Α Α	. А	667 563 763 708 589 608 581 657 717 497 685 540 681 675 627 1641 686
AA950937 A1113626 AA978719 A1260802 A1541593 A1541599 AA695052 A1107772 A1113621 A1515548 A1532198 A1389024 AA391063 AA940727 AA802232 A1531980 dmlf cDNA only AA264488	668 564 764 709 600 596 592 653 718 498 696 541 682 676 628 1642 687	Α	C A	A A	С	Α Α		· T	А	C	C #	<b>A</b> A	т.	Т	C		c	СА	. А	A	т,	A C	A	T (	ЗΤ	Α	А <sup>-</sup>	ГТ	С	G ·	ТА	. А	G .	G (	C C	: т	Α	Α	G		. А	667 563 763 708 599 608 595 591 657 717 497 685 540 681 675 627 1691 696
AA950937 AI113626 AA978719 AI260802 AI541593 AA695052 AI107772 AI113621 AI515548 AI389024 AA391063 AA940727 AA802232 AI531980 dmlf cDNA only AA264488	668 564 764 709 600 596 592 658 718 498 696 541 682 676 628 1692 697	A	т	ŝΤ	т	AA	A C	: G	т	G /	Α /	\ Т	` Т	Т		А <sup>-</sup>	T 1	ТА	Α.	А	Т (	€ G	т	Α ,	А Т	Т	Α (	C A	т	т,	а т		A	т,	A G	ìΤ	A	Α	A	Α &	. A	667 563 763 708 599 608 585 591 657 717 497 685 540 681 675 627 1741 696
AA950937 AI113626 AA978719 AI260802 AI541593 AI541599 AA695052 AI107772 AI113621 AI515548 AI532198 AI389024 AA391063 AA940727 AA802232 AI531980 dmlf cDNA only AA264488	668 564 764 709 600 609 596 658 718 498 686 541 682 676 628 1742 687	A	Α #	A A	A	A A	\ A	. A	A	Α /	55 77 75 66 55 66 74 66 66 66	67 63 63 69 69 69 69 69 69 77 79 79 79 75 75 75 75 75 75 75 75 75 75 75 75 75																														

#### FIGURE 13A

hTPR2 Protein 484 amino acids

MAATEPELLDDQEAKREAETFKEQGNAYYAKKDYNEAYNYYTKAIDMCPKNA SYYGNRAATLMMLGRFREALGDAQQSVRLDDSFVRGHLREGKCHLSLGNAMA ACRSFQRALELDHKNAQAQQEFKNANAVMEYEKIAETDFEKRDFRKVVFCMDR ALEFAPACHRFKILKAECLAMLGRYPEAQSVASDILRMDSTNADALYVRGLCLY YEDCIEKAVQFFVQALRMAPDHEKACIACRNAKALKAKKEDGNKAFKEGNYKL AYELYTEALGIDPNNIKTNAKLYCNRGTVNSKLRKLDDAIEDCTNAVKLDDTYI KAYLRRAQCYMDTEQYEEAVRDYEKVYQTEKTKEHKQLLKNAQLELKKSKRK DYYKILGVDKNASEDEIKKAYRKRALMHHPDRHSGASAEVQKEEEKKFKEVGE AFTILSDPKKKTRYDSGQDLDEEGMNMGDFDPNNIFKAFFGGPGGFSFEASGPGN FFFQFG

#### FIGURE 13B

hTPR2 cDNA 1756 base pairs

CGGCTGCCGCGGAGTGCGATGTGGTAATGGCGGCGACCGAGCCGGAGCTGCT CGACGACCAAGAGGCGAAGAGGAAGCAGAGACTTTCAAGGAACAAGGAAA TGCATACTATGCCAAGAAAGATTACAATGAAGCTTATAATTATTATACAAAA GCCATAGATATGTCCTAAAAATGCTAGCTATTATGGTAATCGAGCAGCCA CCTTGATGATGCTTGGAAGGTTCCGGGAAGCTCTTGGAGATGCACAACAGTC AGTGAGGTTGGATGACAGTTTTGTCCGGGGACATCTACGAGAGGGCAAGTGC CACCTCTCTCTGGGGAATGCCATGGCAGCATGTCGCAGCTTCCAGAGAGCCC TAGAACTGGATCATAAAAATGCTCAGGCACAACAAGAGTTCAAGAATGCTAA TGCAGTCATGGAATATGAGAAAATAGCAGAAACAGATTTTGAGAAGCGAGA TTTTCGGAAGGTTGTTTTCTGCATGGACCGTGCCCTAGAATTTGCCCCTGCCT GCCATCGCTTCAAAATCCTCAAGGCAGAATGTTTAGCAATGCTGGGTCGTTAT CCGGAAGCACAGTCTGTGGCTAGTGACATTCTACGAATGGATTCCACCAATG CAGATGCTCTGTATGTACGAGGTCTTTGCCTTTATTACGAAGATTGTATTGAG AAGGCAGTTCAGTTTTCGTACAGGCTCTCAGGATGGCTCCTGACCACGAGA AGGCCTGCATTGCCTGCAGAAATGCCAAAGCACTCAAAGCAAAGAAGAAGAAG ATGGGAATAAAGCATTTAAGGAAGGAAATTACAAACTAGCATATGAACTGTA CACAGAAGCCCTGGGGATAGACCCCAACAATATAAAAACAAATGCTAAACTC TACTGTAATCGGGGTACGGTTAATTCCAAGCTTAGGAAACTAGATGATGCAA TAGAAGACTGCACAAATGCAGTGAAGCTTGATGACACTTACATAAAAGCCTA CTTGAGAAGAGCTCAGTGTTACATGGACACAGAACAGTATGAAGAAGCAGTA CGAGACTATGAAAAAGTATACCAGACAGAGAAAACAAAAGAACACAAACAG CTCCTAAAAAATGCGCAGCTGGAACTGAAGAAGAGTAAGAGGAAAGATTAC TACAAGATTCTAGGAGTGGACAAGAATGCCTCTGAGGACGAGATCAAGAAA GCTTATCGGAAACGGCCTTGATGCACCATCCAGATCGGCATAGTGGAGCCA GTGCTGAGGTTCAGAAGGAGGAGGAGAAGAAGTTCAAGGAAGTTGGAGAGG CCTTTACTATCCTCTGATCCCAAGAAAAAGACTCGCTATGACAGTGGACAG GACCTAGATGAGGAGGCATGAATATGGGTGATTTTGATCCAAACAATATCT TCAAGGCATTCTTTGGCGGTCCTGGCGGCTTCAGCTTTGAAGCATCTGGTCCA GGGAATTCTTTTTCAATTTGGCTAATGAAGGCCAACCACCCAGAACCCAG AAAATGCAGATTCACTCAGTTTAATCTTGAATGTGGAAACAGTTCACCTCCTC CCTTCATCACGTCTCCGTGTGCTTAGAGCAGTTTCGTTTTCTCAGTTGGATGCC CTGTGTCTCTGTGAGTGGGGTGGAGCAAAGGGAACCAATGCCGAAGACCGAG GGCAGGGGAGGGGGGGGGGGACAGGGAGGCAGCTTGTGAATTTTTGT 

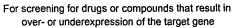
#### FIGURE 14 A

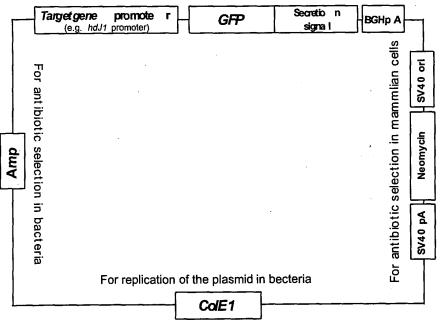
hMLF Protein 268 amino acids
MFRMLNSSFEDDPFFSESILAHRENMRQMIRSFSEPFGRDLLSISDGRGRAHNRRG
HNDGEDSLTHTDVSSFQTMDQMVSNMRNYMQKLERNFGQLSVDPNGHSFCSSS
VMTYSKIGDEPPKVFQASTQTRRAPGGIKETRKAMRDSDSGLEKMAIGHHIHDR
AHVIKKSKNKKTGDEEVNQEFINMNESDAHAFDEEWQSEVLKYKPGRHNLGNT
RMRSVGHENPGSRELKRREKPQQSPAIEHGRRSNVLGDKLHIKGSSVKSNKK

### **FIGURE 14B**

hMLF cDNA 1116 base pairs GTTATGTGTTCCCGTCCGTACTGGAGGCTAGCTCTTGTCGCGGCCGCGCGAG TTAACATCGTTTTTCCAATCTGTCCGCGGCTGCCGCCACCCAAGACAGAGCCA GAATGTTCAGGATGCTGAACAGCAGTTTTGAGGATGACCCCTTCTTCTCTGAG TCCATTCTTGCACACCGAGAAAATATGCGACAGATGATAAGAAGTTTTTCTG AACCCTTTGGAAGAGACTTGCTCAGTATCTCTGATGGTAGAGGGAGAGCTCA TAATCGTAGAGGACATAATGATGGTGAAGATTCTTTGACTCATACAGATGTC AGCTCTTTCCAGACCATGGACCAAATGGTGTCAAATATGAGAAACTATATGC AGAAATTAGAAAGAAACTTCGGTCAACTTTCAGTGGATCCAAATGGACATTC ATTTTGTTCTTCCTCAGTTATGACTTATTCCAAAATAGGAGATGAACCGCCAA AGGTTTTTCAGGCCTCAACTCAAACTCGTCGAGCTCCAGGAGGAATAAAGGA AACCAGGAAAGCAATGAGAGATTCTGACAGTGGACTAGAAAAAATGGCTAT TGGTCATCATATCCATGACCGAGCTCATGTCATTAAAAAGTCAAAGAACAAG GATGCTCATGCTTTTGATGAGGAGTGGCAAAGTGAGGTTTTGAAGTACAAAC CAGGACGACACAATCTAGGAAACACTAGAATGAGAAGTGTTGGCCATGAGA ATCCTGGCTCCCGAGAACTTAAAAGAAGGGAGAAACCTCAACAAAGTCCAGC CATTGAACATGGAAGGAGATCAAATGTTTTGGGGGACAAACTCCACATCAAA GGCTCATCTGTGAAAAGCAACAAAAAATAAATAGCCATGCATTTGATTTGTT TAGTTTTGATTGTTTTAACAGTTAGTAATGGTGCTGGGTAATAAGCATAAGAC CAATCTCTTGCTGTTAAATCAGTTCTGTCCTTGGCAACTTTCTTCTGATATCTG AATGTTCATGAAGGTCCTAGCTTTATATTGTCCCTCTTTTAGGAATAAAATTTT GATTTTCAACAAAAAAA

# FIGURE 15





#### FIGURE 16

dHDJ1 5' region, 24333 base pairs

TTACGGTTTATTTACTATTACTCTAGTTAATCAAATAAACTGTATAATTCCTGG TCTCCGTCGTATTCATCATGGTACATATTACATCCAACATACTTTATTTTTTT GGGTTATTAACATTGGCAATATCGCTGCTCGCCGCCGTTCGGTTATGCTCTAT AAATAAAAGGGGGGCGCCCCTAAAATTATAATAAAATTTTCATGGGTCCTAA ATCTAGTCTCGAAATCTATGTACAAAGTTTGCTTGCATGCTGGTTAGGCATAG GTTCTTAACGTATTATTGGGTTGCTTTATTTCCATTCTGCGCAGTTGTGCAGCC TGTTTAGTGTTTGCCTTTACGGGGTTAACATTTTTTAAAAATGAAACATTAGA GCGGTAACCTTGTTGTCTGATTATTGGCGTCATTAAAGCGGTATCGCCAGCAC GCGATTGATGCAAGGATACCGATTCAATGAAATAAAAACGAATTCAGCCAAA CACAATCTTTCATTTTTTTTTTTTTTTTATCGTACTTAATGATAGCCTTAGTTTCTA ATGGGACTGTGTGCTTCGGTGAAGGTTGGGGATGATTTTGGGAGGCAACAAT TATGTTCTAGCTTATAGCTTACAGTCCTACGCCTACTCCTATTTCTAATATGTT CATCATCAGCAGTTAAAAAACGTTTACAAAACTCATGCGAAATTGAAATCCA ATAACAAATGCACACGCCGCAGTCGCATCGGCGTCATCTCTTTCTCCTGACCC TCGCCTATCCGCATCCAGTTAGGTTTGCTGCTGCTGCTGCGCCGACGGTTGTC GCCGACTGAAGCCACCGCCGGCGGACAGATGTCGTTGCAGGGCTCGCTGCTG CTGGAACTTGGCGCTGCCTGGTCCTCCGAAGCGGTTGAACTTGAACTTGTTGC GCTGCTGGAAGTTCTGGCGATAGTTCTGATTGTAGAATCGCGGAAATCCTCCA CCTCCGCCGTTCTTGTTCCAGCGCTTCTGGCCCTCGTACTCCTGGAATGGATT GTACCCGGGCGTGCTGTTGCTGGCATTGTTTCCCTTAGCCGAACCGGACTTCA CCTTCCGCTGACGTCCACGATCCATCTCGTTCTTCTTCGTCGTCGTCGATGTCCC GCTGCCGCTGCTCACGCGCATCCACCAGTAGCTACGGAAAACAGAATATCAA ACAAGCACTGGGAATATGCACATTGTATTCGAAATGGGTGAGTGGCTTACGG TTCACGGTTCACTGTAACAGGTTATCAGGCAAAACGGTAACGGCACAACGGT TGAATTTATGGCGTATCAGGCGGTTGAAATGAAAGAAACAACGTGCCGGCCA GCAGTCAAATCATAAGCTTCATTGCACGGGAAAACGGATGCGGAGTCATCGG GTGAATTACCTAGGCTCCGGTGCAGTCACTCTCTCCCGCAATGACTTTTGCAA CTCTCTCTACACTTTTCACGCTCGCTGAACGGAGGACGCGTTGTGGTGACCGC CCGGTTGGGAACGGATACCAGCAACGCAGCCATCACAGACTATTCGGGGTAA TCGTATTATTTGTATTTGTTGTGTGGTATGTGCTTAGTGGGGAAAAAGAAG GATCCGGATCGGGTGCGTCAGCGGTCGTGTCTGTTACCGCCACTGCAATTACG ACCACATCTTTACTGTCACTGCCACTAGTCACTGCCGCGTCGACTGCAACCGA GCCCTCGACGATATCGCTGCCTTCCACACTGCCGTGACCAGCTATCCGTTTCG CACAAACCAACTCAAAAGTCTAAATGAATGGGGGATAATGTGGAAACAAATG CAAATTACAAACAAGTTCGTTTAGTAAATCAACTCAATCGAATTGCATTTTAT GCAACAGCTAAGCGAACGACATAGAAAAACAAAAAAAAAGAAGACCAAAGAGCCA GTTAAATAAAGAATTAGTTAAACCCGCAAAAAGAGAACCAATTTATGTA CATTTCATCGTATTAAGCCCGCAACTTGTTATTTTTGAAGCACAGACCCAAA GAAAGTGTTAACCATGCATAGATTTAGTATCTACGTTAGTGACATGGTCACA AGGGATAGATAAGCGCTTCAAGGTGAATGCCTCTCTAAACTCACCTCCTTTTC

GAGCTCCGCGGGCTTGCCATTCCAACTGAGCACGGGGGAGCCGTATCCACGA TACGATTGCTTCAGCAGCTCATTGATGGTGCTCCCATTCGAGGTGGCATTGCT CTGGTAGCCATTGCCCACCCTTGGCTGCTGCTGCGACTTGAGCGCACTGCCGT TGAGCAACTTTTGGCGCTTGGCGCTTGCGGGCGAGTCCGTGGAGGG CTTGCTACTCGAGAAGGGATTGCGATGGTTCTTGTTCGGCGTCGGAATTTTCA CCGGCGATCCCTCCACCACCACGACGTCAACATCATCTTCGATGGCATCGAC CTCATCGTTACGCGTAACTTTCCAGATACCCGTTTTCGATTTGATGACCGCTG GCGAGGGTGCCTCTTTGGCGATGGTGCTTTGCTTTGAGACTGTGATTGC TTCTGTGGGTGCCAGCCATTCGTTAGCTGAATGCTGGGCTCCTCCTCATCGTC GTCCTCATCACTGTCTGCGGACTTTTTTAGGCTCTTGAATATCTCGTCTATGGC ATCAGTCTTTTGTTTGCTGTTGTTAACGTGAACCGATGACGAGGCTGAGCCGT TGGTGTGGCCATTGGTCTTACTGTGACCATTGGTCTGGCCAGACTCTTGG TCCGACTCGCTAGAATCCTCCCCACTTGGACGCTTGCGGGGATTCGGTAGAG GCGCCTCCTCCTCAGATGCTGATTCGTAGGGCACAAGACTTTTCAGTGGC GTTTTGACGGGAGTCTTTACTTGAATCTTTACAGGAGACTTTGCCTTAGGCTC CGTATGATTCTCCGTCATATTGGGCATGCTCGGTAGCTGGGCTGTCGTTGGTC TGGGCTTCATCTCATCCTCGATGTCTTCATCATCCGAGGAAATTGGCAGATAT TGTTGCTGGTTTATTGATTTATGGTTGCTGCTGCTGCTGCTGCTGGGGAGGA ACTTTTGTTACCATTTGCAGTGGGAGCTGAAGTAGCTTCGCCTTTAGCGTGAG CGCCAACCAGTGGAGGCTTCGCAGTGTCCTGAAACTTTCCGGTACCCAGCTG GAGTCCGTTCTGTGGACTTTGCTGGTTTTGTTGCTTGAACTGGATGGCGGTTTT CTGGGCATTTCCATTAGTGTAACCGTTTGCTCCACCCGCCGGCAGTTGAGGAC CAATGAAACGCGTTGGTGAAGGCGAAGACACAGTCGCCGCCGGCACTGGCGT TGTGCTGTCCGTTGGTCAAACGCACTCCATTGGGCCTGTTGGCCGCCGGAC TGGCAGCCTGTGAGAGGTCCAGTTCGAAAAACATTATATAGGCATTTGTGTT GCACACACTGTGCATTGCGATTGGCCGCACGTAGCTGTCGTCGAAGTTGTAA AAGCTGCCCGTATCCGTGGAGCCAATGCCGTGTAGTGACCGCAGTGCTGGG ACGCCCCAAGTGAGTGACCATCGACACCAGGCGATAGGTGAGCGGTTGAGC CTGAGCTGCTTGTGAACGGGCTGCGTATTTGCTCAAATCTATGCGTGACTTGA AGGAAATCTGCTTGGTCAGTTTGTTGCCGATCATGGAGAATCGCTTCAGCTGT ATACAAAGCGTGATTGGGGCACGCTCCAAAGAGAATTGCTTTGTGGCAGATA CCTGCAAGCGATACGTTTAAATAAAATGAACTACAGAACAAAGGTCACAAAG ACCTACCTTCTTGCATCCCTCGCACTTGTAGCCCATATCCTCTAGCCGTTC GCGAGAAAGTGTCCCTCGAAAGCATCCTCCAAGGAGTCTGCCTTGCGGATG TCGAGCAACAGATCCTGGAAGTGCTGAAACGTAATGGACACATGGTTGCAGC TCAGACAGCGCACCTCGCTGCGCAGATAGCCGCCAAAGATCTGTCCCAGCGG CGTGGTCTCCTTAACCAACTGATCCAGCTCTTTGTAGTTACGAAACCGCATCA AATACGCCCGCTCCATGGCCTCGACCAGGAAGCGCAGGAACTCGTGCGCATC CTCTTGGCGACCAACGACCATGTGTTTGCAGATCTGCTTTAGCTTCGAGTAGA TGAGGAAGGGTCTGACGGCCGACTGATTGCTTTGGGTGGCCAAAAGTGTTTT GGTCATGGCGCAAATGATGCAACCGCTGCCAGGTTCGGCCACATTGCAGTCA GCCAGATGCGCCTGCTCCGAAACGAGCCAATTGGCCAGGGCGGGTATGTGCA GGAGCGCCTGAAGCGTTGAGTTGAGGTAGCAGGTGTTGCCCACATTGATCAT GCCCGTGCCCACCTGCCATTTGCGCTCCGACTGCTTCCAGCCAATGCGTATGT TCTCCCGCGGATAGAGGACCCTCTTCGGCTTGGGCAGCTCATTGGGATTGCTT GTCGGATGCTGATGATTGTGGTGGTTGATGTGCGACTGATTGTTCGGGTG

CTCCGCTTGCTGCGGGCGCCGTTATTGTCTGCAAAGGTAAAGAGGACGGTA GACAGTTTAAGCACGTGCCACAGGAGAAGGCAGCAGGAGACAGGAACAGC TTGTAGAGCAGCCACAGGGCGAACCCGTCCACCATTATCACAGTCATAATGC ATTTATTGGAAGAATTCCCTTCTGCAGATTAAGTCACTTGATCCGCGCTGCTA TGAAATATAAATAAACGAGCAGTGCTCGCTGTGGAAACTGCTGACACAA TCGCGCTTCCATCACCTGTTCGCAGTGTTGGAAAGGGTACACATTTGTTGTAC CTAGGCACCGGACTGTGCAGCATTAAGATAGCTATTCTATTGAACAAAGAAA CTTGAACACAAAGTATACGCCGAAAAAAATTTCCAGTACTAGATTTTGAAAT ACAATTCTTTGAACATCGTTACAGAATGTGATATCACCAGATTTTATCTGAAA ATATTTCACAGCATCGTAATTTCATATGTACCCTGAATATGTATCTTGCAGTT TTGTTTGGGAAAGTGTACCAATCGAGGTACTTATCCTGGTACACATATCTCAG ATATTACCCAGCACTATTGTATCTTTGATAACAGCTAGCGTGTGAGCGGGATG GCGACTGGCAGAAGAAGAAATTTAAACTGATAACAGCAAGCGAATGAGAGG GATGGCGAGTGGTGAAGCAGTCCAAGTGTCTGCCGACGAATACAGTGGT CTCGTTCTGGCGTAGGGGGTTGGGGCGGCAGTGTTGCCAACTGAATTTTTGGC GCGACCTAACAGTGGTTGTTGTAGGCCCAATGCTCCCCCCTTTTATTGTCTTT AGTCGAAACATCGTGTAACAGCTCCTGGTGCTGAGCTTTGTGTCCACTTCCTG AATAAAAGCACCGCTGGGGCTGGCCATGTGCGGGGAAAGAGAGACGAACTA CGGAGGGGAGCCCTCGTGCTTTTTGTCTTTTTTCCTTCTTTCATTTGCCGCTG GAAATACAGCACGTTTTTTTCCGCCACAACTTCTGTGAATCAGAAGTTTGGAA GAGGCGCTCTGTTGTTGCTGCTGCTGCTGTCACTTTTCCAGCTTACTCTTTAC GGCGTTGTACTTGTTTTGCTTTTTCCGCGTATTCCTTTGCATTCTGTTTACACG ACAGAAGCGCCTAAAAAGTACAGGTATGCTGCGCTGCCGACGTCGACTGCAC TGCCGACAAAATGCAGGCGGAGCAATAAAAAAAATATGTTTGCGGAAAAAC AAGATATAGCACATGGAAAATTGCGCAAAAATTGCCACACAAAGAAGAAAC TTACATTTTGTTGTATCTTTACACAGTGTACTCACCATGTCCATTTGCGCCCAC AAGTTTGCCTGTATTGTTTTTGCCACTAAAGCCATTGATGGCGCCTGGATTTC CCGGCTTGATGACAATATATTTGGACTTGAGGTTCTCCAGCACCGATTCGTGG TAGTTGGGCACCTCCTCGTATTCGATTTTGGCCATCAGGATGCGTTTGGCATT GGCCACGATGTGATTTTGCAGGCTGCCGTTGGTGTCCTCGCCGCTCTTGGCCT GGTCAGTCGACGAGCCGGCGGAGGAGTTGCCGCCAAGGGATTCGCGCAGCG CTGCGTTGACGACATTCGCCGTTTCGCATACGGCCATCGAAACGGGCATGGC GATGCTCCGGCTGGGATTTGCGGTGGAATTTTGAACGGGTGTGAGGGGCGT GGTGTGGCGTGTTTGGTGGTTTTCGCCACCCAGTTAGCTAATGCACATGGGC GTGCGATCCAAAGCAGATACTAGAGATCCTTCTGCACAGCCCACACGTCCTT CAAAACTCTCCTACTCTACGCTCACTTTTCTCCTCGCCCCTCTCTCGAACA CTTCTTGTTTCACACACCGACTGCGACACCGACACACGCACACTAACGCACTC GGGAGCACTCTTCTTTTCTGGCTTTTTCGCGCTGCGATCTCGATCTGTTGGCC TACTGAGCATTACGATTAAGAAACGTTCGCTCACAAATTGATCTGTTTCAATT

TCGTGCGCGGCCAGGCATTTTAGAACGAAAAGTCTGCTTTCGAAAATAATGG CAATTCCTTCCCTCGTGTTTCTTCCGACTGCGGATTCTCTTTTCGCTTCATTTTC GTCATTTGGGGATGCCAACTCGCGAGTGGCCAAGTGACGCGATAGGCCTCTC GAAATGTCCTAAAGCATTTCACGATATTTACAAAAATGTATTTCGATGTTTTC TTAACAATAAAAATTGGTTTAAATTTAATAAGACATTTGTTACCTTGAATAT TATTCAAGTTATAAATTTAATTTTATAACGGTATTTTTACACCTTATCAGCAC ATATCGATAAGTGTGATTGGGAACGACAACCCATCGGCACAATGTTGATGCA ATTGTTGAGCTAGCCTTCATAATTAGTCGCAATCAATCGAGCAGAATGGCTTC ATCCACAGGTCTCCTGGTGTGTCCAACATCAAGCACCTTGGCAAATCCCTGC GAGCCATCGAGAAGTACGTGAATTCACTGTACATCCACCTAAATGTGGCGGG GTCAACGTCCACGACGTCACCAGTTCCACCGCCTCCGGTTTGGGGTCGTCTAA TCTCGCAGCTGTACGCCAACAGCAGCAGCTATGTGGGCAAGCAGTTGGACCT TCGCGTCCTTGTCTCCCCCTACGACCAGGTGCCAATGGATCCCTGAAGTTGC GCCAGCCGTCGACCTAATCTTCTCGGATGCACATCATCCGGAGCTGTGCGAC AGGCTTCGCGCGGATCTTAACATCAGCAAGCCAACAATCTTCCTGGATGACT CGGTCATCTCGGATTTAAGTGCCCAGCAGGATGACACCCAGCCGCCTAAGGT AGATATTCCTCACCCAGGCTGTACTGCGCACCTGCAAGCGTTTGGTTGTGGGC GTAACCACCTCCGCCATGACGAAGGGTAAGACGGGCATGAATTGGCAAAATA AAACGCTTATCTTAACGACCATTCTTATCGCTGTCTGCAGGAAAGACGCTGCC GGACTTGATTTTGCCCGTGGAAGAGCGCATCGCCCGGCTAAGGGAGTTCCTG GTGGACATAGATGATACGCTGCAGTACGAAATTGTGCCCATCGATGATCCCT TTGGTCCCACGCAAGTGGATCCTGACCTGGACATGATTGTGGTCAGTGCGGA GACGTTGCGAGGAGGCAGAAGGTCAACGAGGTACGCTCCGCTAAGCAACT GCGCGAGCTGGAGATCTTTGTGATTGACATTGTTGAAAGCAACGTGCATGAT GGCATCCACGAGACCAAGGTCAGCTCGAGTAACACACGCATCGATCTGCTGG GAACCCGCTGGAGAAGGCCGGAGCCACGACCACAGCTCCCGCCGCCCCTTA CATTATTGGACTCACTGGCGCATCGCATCTGGCAAGAGCAAGATGGGCGAG AGATTGGCCAACATGGGCGCCCACGTGATCGACTGCGATAAGGTGGCGCACG ATGTTTACGAACCTGGTCAGTTGTGCTACACCCGAATTGTGCAGCACTTCGGA CAGGGTATTGTTTCAGACGATGGTCGCATCGATCGGTCCAAGCTGGGACCCTT GGTGTTTGCCGATCCCAAGCAGTTGCAAGCACTCAACGGCATTGTCTGGCCG GAACTTATTGCGGAGGTTAACAGGCGGCTGGATGCACTGCGTTCCCAGGCGG ACGTGCCGCGTGTGGTGGTCCTGGAGGCAGCGGTGCTGCTGCGAGCGGGCTG GGAGACCAATTGCCATGAGGTGTGGTCCATGATTGTGCCACCGGATGAGGCT GTGCGGCGATTATTGAGCGCAACAAGTTGAGCGAAGTGGAGGCCCAAAAG CGACTGGCCAGTCAGGTGCCCAATTCTGAGATCGTGGCCAAGTCGCATGTGA TATTCAGTTCGCAATGGGATCACGAATTCACCCAGAAACAGGCGGAGCGTGC GTGGAAAATGCTTACCAAGGAACTGGACTCTTACCAGAGCAGCCTTTAACCC GATGGATATTTAGATTATCTTGTTGATCCTTATTTTGTATGATTTTTTATGCAT TTGTTGTATATTGTTTAGTTGTAAGTCCAAAGTTGAAAAGAAATGCTGGGACG TCATTGGGGAAAAACGCTGAAAATTTCAATGGAACCTTAGTGGCTCTCGCCC TTCTTGCCAGCCACTCGCTTGAAGTCGTTCATCTTGGTGGTCATGATGGGGGA TCTTCACGAAGATTTGGATGTTTTGCACATTCTGGAACTTGACGTAGCGCAGA

TTCACGGGCACTCCACTCTCCAGCTCCTTCTGAGCCAGGCTGCAAAATGGATT GAACAGTGAGAAGAGCTAAGCAGCCATAGAGAAGGCAATAGCTACCTTAGA TCCTGCACACTGTTCATGGACTCGGCCATGTCAAAGTCAATCGTGCGGGGCTG GTTAATGAACAGCTTCACATCCTTGGGACCCAGGTGCGAAGGTGCCTTGAAC TTCAAAGAGTGGATCTTCACAGCCTGATTAAAGGTGATGGACAGGATGAGCT GCTCATCGCAATCGGACTGCAGGTAGCCACCGGCGGAGGCCAGGGCGTGCTT TAAGTTGTGGTCATCAGCTTCGTTGAGGCACTCGCACTCCTGCTTCGAAATAA ATGTATTCAGTTCCATCTGTAAGAAGGATTAGGGATTATTTTTGGAACATTTC CAAATACTGCACTATATTACCAATCCCTGCCCGTAATCCTCGCCCCCCTCCTC GCCACCGGATGTACCGATGTGCTCCTGGATCTTGGCCTCGAGCCCATTGACGT CCGCACCCTGGACGCGATCGATCTTGGTCCTGTTCCTGTAGAAGATGAATGTT GGCATGGCCGAAACGCCCTGTCCAGCAGCCGTGTCCTGGCACTTGTCCACAT CCACTTTCAGGAAGATGGCCTTTGGGTACTTTGTTGGAAACGTCTCGAAGATG GGCGCAATCCGCTTGCAGGGACCACACCACGAAGCTGTGAAGTCCACCACAA CCAATTGAATGCCCGCTTGGGCCAACTCCGCCTGGAAGTGGGACTCGTCGTT GATCACGCGCACGGACATGGTGATAGGATTAGGTTTCTATTAATTGAGCTTTT GTTTCGGCAGCCGAATTGGATTTAAGCAAGTAAATGTTATTATTAACGTTCAA TGCAAATTTTTTTTTTTAAAGATGACTTGTAATATGCATTTAGTCCAAATTCGT GCTAAGAAAATACCGAATGCGGTATTCCACAAGCGGTCACACTGTGATGGT ATCGATATTTCGAGCTCTTTGACTTCCTATTTTTAGAGGGACCATTTATGTGTA ATAGAAAAAACCGAAACTTAATATTTAAACTTTTATTGAAATATTAGTGGA TTACAATATGTAAAACTATGAAATATTCTCATTTGATATAGCTCAAAGTGTTA TTTAAAATTCATTCAGTGTTTACGACTAGCAATCTACGCTTTCACGCTCATCTT AAGCTTACCGCCCATTTGCCAGGGTTGTCAAGGCGAATGAGCGGTCCCACCA TACACGCCACTGGAACTTTCGATACCTGCGCTGCGCCTGGCCACACGTTCATT ACCTCGTGGTGTTTCAGTCGGTCGCATTTTCATTAAGTCGCCATTTTAAAATT ATTAGAGTCAAGTACAATGGCAGATGTGGAAAAGGAGCCCGAGAAGACCAT CGCCGAGGATTTGGTGGTGACCAAGTATAAGTTGGCCGGCGAAATCGTCAAC AGTGAGTATTCCTTGGCCGGAAACAGCGAACGCTGGCCGATTCCTGGAGTCG CTGCTACGTGGCGCTTACACAATGCACCGAATGCCGCTTTCCCTTGTGCGCCA CGCGTTGGTTAATCTGCCTATTTCTGGACTCTGTCTGCTCGTTTAATTTTAGAA GTGGCCACCTGGCGGTCATTCGCGCCAATTTCATGTCCAATGATTAAGACTTA CACCTTTGAGGGTTTCCCGATGGCGAGCCATGTGCTGTGCGGGCTGGGGATC ACCTCGTGGTCGCCAGGCGCACGCGGGGACTCCAATGCTCCACGTGCCCGGC TTGTGTGCTCTCCAAAAGGTCCCGAGGATTTACAGATTATGAGATCTGAGGA CACACCGCGCACTATCATTGATATATAGTACAACGAACAAGCAATCTAATGC TTTTATCGATCTTTCACAAACAGGTATACAAAAAGGAGAAAAAGACCTGAAGAA GGGCATTGCCTTTCCCACCTGTCTGTCCGTCAACAACTGTGTCTGCCACTTCT CGCCAGCCAAAAACGATGCTGACTACACGTTAAAGGCCGGTGATGTGGTCAA AATGTAAGTTGAACCTCCTATTCCACATATACCGCCACTAAATACGTAACATT TCTTTCTACAGCGATCTGGGTGCCCACATTGATGGTTTCATTGCCGTGGCCG CTCACACAATTGTGGTAGGCGCTGCTGCGGATCAGAAGATCAGTGGTCGCCA GGCCGATGTCATCCTCGCCGCCTACTGGGCTGTCCAGGCTGCCTTACGTCTGC TCAAGTCCGGCGCCAATGTGAGTCCTCCCTTACTTCTAGGTAATCCTCCGTTA

ATCCCTGCAAGAAACGGATTGTCTGCCGCGATTCTCCAGCGACTGAACATCTC AACACTTGCAAAGATCAGCTGTGGCAGCTGGTAATTGCCCTGGCCTATTATTC AGGACTGGAGGCTTCTTGTCAGTTGTCCACAAGGTTATTTCTTCTGCAGGCAA CGGATTGACTGCGCTCAAACTCTGACACAGATCAGCTCAACACCTGCGGATA GAAACTGTGTCAATTTCGTGAACTGAACAAGTTCATTCCATAGAAGTGTTCGG TCTTTAAATTTGTCCACATCTCCAGTTTATAGATATGTCGGAATTGTAATCTGC AGGCAACGGATTGTCTGCTGCCTTAACTCGTGGCTCAGCACAGCTCAACGTCT GCAGAGATCAACAGTGTCGATTTCGTGAACTGAACAAGTTTAGATACTTGAA ATGTTCGGTCTTTAAAGTTGTCCACAATCGCAATGATAATGCCGATCAGTTAT TGTTATTTTGCGTTATCTATAGTATACTATGATATTTGATTAAGATTAGTCAAA GGGAATTGGAATGTTTTCTTTATCTCTGCTTTGAACTATTTCCATTTTATTTCA TACTTAATATTTATGTTTCAATTCTGTATCCTTACAGAACTACTCCCTCACCGA TGCAGTGCAACAAATCAGCGAGTCGTATAAGTGCAAGCCCATTGAGGGCATG CTCAGTCACGAGCTGAAGCAGTTCAAAATTGACGGCGAGAAGACGATCATAC AGAACCCCAGCGAGGCGCAGCGCAAGGAGCATGAGAAGTGCACCTTCGAAA CGTACGAGGTGTATGCCATCGATGTTATCGTCAGTACCGGCGAAGGAGTGGT TAGTAATCCATCAATAGACACTACATCTCCACTAATTTGTTCGATGATTAAAA CTTGTTTGCTCGGCGTTTTTTTATACTAAAATGCGGCACGTGCAGACACCAAG TTCCGGCTGGCTGTTCCGAAGATTGCAAGATTATGAGATCTGAGAACGCC AAATTTAAGCTGGATCCTGGATCATCGCAGCCAGAGCATTATTGCTAACATTA TTCGTATTCGTTGCAGGGACGCGAAAAGGACACCAAGGTCTCAATTTACAAG AAGTCTGAGGAGAACTACATGCTCAAGATGAAGGCGTCCCGTGCTCTGCTGG CAGAGGTGAAAACCAAGTACGGAAACATGCCATTCAACATCCGCAGCTTCGA GGAGGAGACCAAGGCCCGCATGGGAGTTGTTGAGTGCGTCGGCCACAAGAT GATTGAGCCCTTCCAAGTGCTGTACGAGAAGCCATGTAAGTGTGATGCATAT TATTATTAATCCTATTCCCTATTATGCGAGTTGGCAGAACTTAATTCCGGACC TGGTACACCTTCGGGTGCTAAGTGCGGCCAGACATTTTGCCAGAACAAATTC CACTGTCACAATCGTATCCAATCTATTAACCTGTTTTCTTATACTTATTAAAGT TAATTTAGAGACTAAACTAGTTTGAGCAACCTTTATAAAGTTCGAATTTTAGC CGGAAGTAATAGCAAAGTTAAACAATCCTTTTCCTTATCTTGCATTACAGCCG AGATTGTGGCGCAGTTTAAGCACACGGTTCTGCTCATGCCTAACGGCGTCAA CTTGGTCACCGGCATCCCATTCGAGGCGAGAACTATGTGAGCGAGTACAGT GTTGCGCAGGAGGAGCTCAAGGTAAGCTGCAACAATTTCCTTGTATTCACGA TGCGTACTCAATGAAATCTCAACTTTTTGCAGACTCTGCTCGCGCAGCCTTTG GGTCCTGTGAAGGGCAAGGGTAAGGGCAAGAAGGCAACAGCTGGGGCGCG ACAAAGGTGGAAACGGCGCCGGCCGTGGAGACCAAGGCATAGACCAGCCCG CTGATGATGATCCGCACCGCCAAGCCATCAACGGAAACACAATGTGAACAAT TGCGCTGCCCAACGCTGCGCTCCACAGATTTTTACTATCGAATTCGTTGCGTA TTAGAGGACCCTTTTGACAACAGAACAGGACAGAAGAGAAGACGGCAACAA CGGTCGGTCCCGCGCCAACTTTACCTCTTTATTTCCTTTACTATAAGCTGCCTT CGTTTATCGGTCTGTTCAACATCATCGCAACGAAAAAGCAAAGCAAGAACTG TCATCAAATTGTAACAATTTTAACGCTAAATGATCTTAAAATATAATTCAAGT GAAACGTTATTAACGCTGCGTAGTAGGTATTAAATAAAATTAACATTTCTAT

CCCAATTTAATTCGATTCGATACGCTTCTCATTCTAATAAATGCACTTGCG AGTTGTGTTTATTTTATACGTTTAATTTAGTTTTGATGTTCACATTCACATTAT ACAATTTGTAATTTAGATTTCTTGCCTTTTGTTATTTTAAATTTTACAGTCTCA TCTTTGAACTCTTGTATTACGAAAGTTGCAAGAATAACTTCGTTATGTTAAAC GTCACTTAGTGCTGTGCTCACTTGGCCACCCCAGTTGTCCATCCCAGATCCAA TCCCAACAGACCAGACCAATTCGATGCCGTATACGGCGACTTTGCCCAACT TTGCTGCGGATGAAGTATAGAAAACACGAGCACCTTGCAGACGACAAAG ATATGTGGCCGGTGATCAAAAGAGGATCTGGGATTTAATGGTCTGCCGTCGC TTTTCTACTCGCCAGACTAATTATTGACATGCACGTCCATCGGTGCGGAGGCG GTCACGTTGCTCGACTTCTCCGGAGAGTCCAGGTAAATCTTCAAGGCACGTTC CCGGCGCTGCGCATACCGCGTGGTGGACACGCAGCCCACCCGATCCAGTCGT GCCTTCTCCCTGGCGTTCATCAGGCGTCGCTCCTCCAGCGTCAGCTCTCGCGC AGGTACCGTCCTATCTCTGTTGAATTCATTGGTTAGTCTAGGAACTGAACTGC AGCGGATATTTGTCCAGGGTGGTGGGCACGGAGTACCAACTGCTGGACTCGT TAACACTTAACGCTGATATGCTTGTGCAGGGGAAGTTGCTGTTCAACTGCAG AGAAGACCAATTAGATCAATATACACAGTAGAACGCAATTTTACGAACCTTC ATATAGCTCAGTTTGTCTATTGGGATGTCGCTGATCTGTGATAATGAAAGTCT GATTTCGCTGTCCTCTGCAGAAGATACGAGTTCGATTTACTGCTTACAGGGCA ATATACAGATTTAACTTACGGTCCAAAGTGATTTCTTGGAACTTTCCAAACTC CAGTTTAGCCGGACACCACCGTCTTACAAATAAAGTCAGAGAATCGTCCTTG GGCTGCGGGTCCACTTCCTCCTCGCACTCTTGCACAATGAACTGAAATGGTGT GATATAAAATCCAAGTTAAGTTTTTTTCTCATCACAGAGACAGGGGAACCCA CCTCCGCTGCGATGCTGGAGCGCATGTCGCAGTAGAGCGTTTCATCGTCGGA CAGAATTTTGATGGGAATACGTCCGCCCTTCAGCCAGATGCGACAGTTTTGCA CAGACAGTGTGGCGTACTTGGCGTCTATGCGATGCAGCTTGGCCACCAGTTCC TTCTTGGCCTGCTCCGCCGTGGTGTTGGCATTGTAGACCCACTCGCATACGCA AGGCAGTTTGGACGTCTCGTTATCAATGTCCGCCAGTCGCAGGAAGTGAATC TTGGCCTTGAACTCGTCCGGCTCCAGCGTCTTACCCAACTCCACCGTCAGTGT TTCGCCTTCTATGAGATGTACCAACGAGTTGTTCTGGTTGTTCGACAGATTAT TATCGTGTTTCCGCTGCAGTTTAAAGTGGGCGGCGGCACTTGGATCAGCTGC TCGATGTGTTTCTTAAAGGCCCCCATTCGCATGTGTGTGCCCACCAGCAGCTT ATAGGCACGCGTGGGCTTACGCAGCTGAGCCTCTTCGTCGGACTGGTGACCA GAACTGGAACCGGTGCCAACCACATCCACGCACTCGACCTTTGTGGCGTAGA AGAAGTGGTTGGTGGTGGGCAGGAGCAGCGGATCCACCACATCGGCCGC CGCATAACTGCCGTTTCCATTGCAGTAGGCATGAACGCGCATCATGGCATCGT GTGAGGCTGCTTCGTCCTCCGGACTAGACAGCTGCGGCGAGTGACTGGTGGA ACTGACTTGGCTGTCGCCTCCACCGCGATGTGCCATGTTGTCCGTCTCCACCA GAGTTCGGTCTCCGTCGCTCAGACTACTGTCCTCCGAGTTGGACTCGTGGCCG TGGCTGGGACTGGGTTGTGACATGGGTTCCACTAGATCTCGCTTGTAGCGCCT CCAATCGTAGTCGTTGCTGGATGACATGTGACCAGGTGCCACGCCATTCATCA TTGCAGCATCCACAACATCACCCCCGCTGGCGCACTGAAAGGACAGCCAAAA 

CGGTGGGCACACCGAGCATCTCAAGGGTCGCGGCATCCGTGTTGGGTACGTT CAAGTAGAAGTATGTTATGGACTTAAACTGGGTGTTGGCCATGTTCTGGAGA TGTTGCAGGGCCTCCGGCGTCGGATGCGGATCGTAGGACACGAAAGCCTTCG GCACCGTGGCGCACCGTGGCGAGTAGGAACTGCTGCTCGCTAATGTGCAA ACGGAGGCGATCGAGCGCGAAGGACGTCGCTGGCTTCCCGCTCCCGCGCT GCTGAGTAAACCAGGAAGGGACCGTCCATCGCCATGGTCGATAGATCTACCT TAAACACATACCAAGTAATGCCGTTCGGCGGATAGACCTCAAACTCTTGGTC CTCGGCCGGTACTCCAGCAGGAAGTCGAGACTGTAGTTCTGCGCCGCGCGC AGTTCGGTCAAAGCTGGGTCTGTGCAACTCTCCAGGGACTGAATAATCGTGT CCATCGAGGAGTTGTAAGCCACCAAACGACAGCGGGAAAGCGGCGCGAATT GTTCCACATTCAACATCTCATAGGCCGACATGAGGACCAAGTTGATGTTGAA AGAAGTAGACGCGCGCTTGTACAAATCCGGAAGAGCCAAGTCCGTAACCGT GATATGCCTGCCCAGGCGGGACACGCGCGTCTCCTCCTCCGAGTGCAGCTTTG GTAGCAGCGTTTTGATGTGCTCAGGAAAGTCGGCCACCTTGGCGACTAGCTC GTTTCTTTTGGCATCCACCTGCCGGTACATCAACATGTATGCATTGGTGCTGG GATGTCCTCTTGGGTGATCTATGGATAGATAGTCGTTCAATATTTTCTCAAGT TATGAATGTGTTGCGAAAACCTACACTAGTCACGTTCTGATCGTTAAAACAG AACCACTCGTTGTTGTCGAAGTCCTTAATATAAGCATAGTAGTGTCCGCCCGA AGCGCTGCCTGAATGAATCATGATGGCGAACAGTTCGTAGAGATACGGACCG GATCCTTGCTTGCTGCTGCTGCTGCTCATGTCGATGCCTTCATCC TCGTCGTTCAGATCGTTTTCGTGCTGACTAGAGCTCGCTGTGGTCACCACGCC GCTGCTCAAATTATCGTCCTCCATGGCGGATCCACTATCCGCCGTGCTGCAAT CGTCCACGGTGCCGTTGAGCTGAGAGTTTTGCTCACCGCTGTTTCCACTTCGG TTAATGAACGTGTTCAGGTTGAGCGTCTGAGGGAAGGTCACTCTGAAATAGA GGGCGAGCATGGAATTAAATGCTTATGGATTATGGCAAAGAGACTAACCTGT CGTTTAATTTGATGCGGTGCATGGTCTGGTAGTCAAAGTCAAAGCGTTTAAGG TGCAGCGTGAGGATGTAGGGAAAGGACTTAAAGTGCAGTCCCTTGTGGGCGT CGCATTTTTCTTGCACTTCTCGCACAGATACTGGTTATTGCCATCGAGTGTTT CGGGCTGAACGAAGGCACGCAGAGCTTCCTCGATGCTGCCGTATGCGGAGCT GCTTCCAAAGGGCCTCACAGGGAGCGGGATATCTAGAAAGGTGTCCTCGCGC GTACAGATTAGAGATGAGATTTGCCTGCTTAGTGTTCTTGAATTTGTGCTCCA GAGCGTCGAACATAACTCGGCACAGTTCCTGGATATCGTGCTGCCGTGCCATGC CTCCGTCGAGTCCCACCCAAAGCTGCGAGTCAGGTCTGTGGTTTCTACCGCCG CTTTGGGCGAGGTCTGCAAGTTGAGGAAGAGCTTTTGCAGTTGGTATGGTAT GTTCTTGGCCTCGTTGTCATTGTCGAACTCCCAGCGGTACAGAGCATTTCTGA ACTCGGGTGTCATAAAGAGTGCCTGCAGCAAGCTGTTTAGATAGCAGGTCAT CCTCTGCCTCAGTTTCTGTGGTGGCCGAGGACACGAAGTCCGCACCCGTTGTG TTGACTCTCTGCCATGCTCGCAACTCATCGCCTCCATACTTGCGACGATAGAA GTTTGACAGAGCCGGGTACGTACCATCGTCTGTTCCAATTGTGGATGGGTCTG TCACTCCGGTCACACCCTCGACGTCCGAGTCACCGGTCGGAGCTCCGTAATC GTATCCAGGTCCCAGCATTGTCGGACTAGCAGATGCTCCGAGTGCCAGGTCG TCATCCGACAATTGTTCAGCATCTGAGATGAAAAGATCTGAAGGAGCATCGT

CCACCGGTGAGATTAGGTTTCTACCTTGTGGATACAGCTGCAGTTGCTCAGAG AGCTGTTGCTCAGGGTGTCTACTGGTTCGCAGTCCAACTCTTTGATGGG TGATGACGGCTTGATTGGACTCAGCAACTCTAAAGTCGGCTTAGAAGTGACC TTGGCCGTTTTCTTGGCCACAGGACTCTCCGAAGAAGTGTTTTTAGAGTTTAT CTCTGTAGACAGCTCGGGACATTCTTCAGGGCTAGCCCTGGGAGCTTTTTCCG AACCGGGCTTGGAGATCTTTGCTGCAGTCGTCTTGATCTTGGAAGTCTTTTCG GGACTTGATTCCGAACTGATGCTGGTCTTAGCCAAAGAGTCCTCACTCGTCGT CTTGGCCTTGCTTGGAGAGGAAGATCCCGAAGCTGGCTTCTTTTCGTTTTCT CACCAACTACGCGTTTCTTCTCTCGCCGGTGGCAGGACTCTTGGCCTTCTCG CCGTCCGACTTCATAACCTTTTTGACTACCACTCTTTTAATGGGTAACTCAAA GCGTTTGGTCACGTCACCATCCCAACTGCCGGAGGGCAGCAGGATCAAGTGA TTCTTCAGCTGGGGCTCAAAACCAGCCACTTCGTACATCAGCTGAGATTCCAG GGCATTCAGATTGACCTAAAGTAAAGGGGAATTCAATTAGCGGTTTATTAGA ACCTCAAGATGTGCAGATATTTTTACCAGATCCTTGTTATCGTGTGGCTGCAG CAACAGCTCGAACTTTTCGTACGAGAACTGCGTGCCAATAAGGTCAATCACG CGTTTCACCGTGAAGTGGGAGCGGACCACTACGTTGATCTTCTTTTGCTCCGA TCATGTCCAGCCCGCGGAATAATCAAGTGATGGTGGAGAAAACCCTGCAAAA AGATTGTAGGCGAAACGTTGGCTTTACTTATGAATTTTGTCTGGAGTTTTCTTT TTATTTTTTTTTTTTTTTTTTTTTTTTTTTTAGAATTAAAAAGGTGACACGACACCTTTG ACGTTTTCGGCGGGGCCAAGTTCCTGGACATGACGATGCTTCTTGGCCCATAG TAAATAAGGAAGAGATGCCCAGCCCCAAATTACTGCGAAATCTTCTTGTTTTC GACCCCATTCGCGAATAAAGCGGCAGAAACCAAGAAGATTCCGTCCCACCTC CCGCAGCCGCAGATATTGACGTGCTCCGGGTTTGCTTTTCGCGCCTTATTTGT ATACACATATAGCACGTACACCCAATCGAGCATCGACTGCCCCCGAAATCG ACGTCGTGACTAACGCGCAGGGGAATTTCGTAAACAACCGGCCATCAGAGTT GCCTCCGGAGGATGCTACGGGAATTATTATTTGCCTCCAATGGACTACCAAC GTCATCATCATCATGACCATAGCTATCACCATCGGGCGTACCGAATGCAT AAATTTCAGTGCAAATGTCGCTCCATGTTTCAGCTGGCTTCCTTTGTGGCTCC GCCTTCAATTCGGCAGTGCGCATATTGCAAGTGGACGGTGGACATATCCATA TGTACAAATTAATACTTATCGGACATCAGCGTGAACACTGCGAATTATTCTAG AAACATTTGTAGAATTCGAAAGATTTAAGGAAAGCAGATGCTGAATATTAGG CGAAAAGCGATTGAACTACTCTATAATATGCAGTCAAAAATATCATCGATTC GCCTGTCAATTAATTGTATCTAAAATTATACTTTTCGAATGTCTATTTTGGCAA GGGGCCGGGTATTTGCAATGTTTTTCCAATTCTCTGCACCGAAATAACCACA AAAAAGACAGCCAGTCAGCCAAGATATTTTGGGTCTCCTCCGAATGGAGGAT GCACATCCACGATGTGCGATGTGAATGCGCTGCAATTGGGCGTTCAAACACA TGTTGGATGGTCCAAACACAAACCGCATTGCCCGGCAAGGGAGCGAGTGAGA TGGGGATCCAAAAATGCTAATACACGTCGGCCAGCACAAAATCAAAATAAG AAACCCATGCTGCTAAAAATAAAAACTGGCGGCGGCGACACAACGACACAT CGGAGCGTCGGAAAAAGCACACAGGCGAGTGGAGGAGCAAGATATAAGAC AGCTTTGGGAGCGTCTTGAATACGCGTATATCTGGCTATTTGTGAATGCGAAG GTTTTTGAGAAATTCAGAGAAGCGCACAGACTGTTCGAATACGTCTATCCTAT

TATTTACATGATGACGATGATCTTTTGGTCAATGTTTGTGTTGGTCGGGTATT ACAGAAACCGATATCGCGAGTTATCTATGCCATATACACGATCCAATGGGGG GACGGCGGAGGGCAACAGTCATGCTCGCATATATTTGTGCTATTTTTGAA CTATTTCGGTACTGCGAAATCTATGTGATCTACAAAAACCATGAGATGTCTGA GATATGACTGCTGAGTGCCGGAAATTGTAGGATTCTCGATTCCCGATCATATA ATGCATTCTCGAACAGAAAATCTCCATTACGAAATGCTTTCTATTCTTAGGCG TCGCACAACTTTAATTGGAGCTTCCAATGTTGTGTGAATAAGTGTGTATATAT CCGTGGTCTATATATGCAACGGATTTTGGTGAGTTTTACCGTCTGTGTCGGAA CTGAGTGTGCCGAAATCTTTCCGAACTAGAAGACCGCACCGTCAACGCACGG CATAGTTCACGCGTGTACTGGCCGCTTAGGATGCCGATGCCGATTCCGATTGC GATCCGAAGATACACCACCCGATCTGGCGCCCGATCTTTGGCGAAGCGAGCT ACGTGTTAAGTTCTCGGCGTGATGTACTATAACAATGAGAAACAGTTTACTTA TCTGGCTTACACTTCAATAGGAAAACAATACTTTTATATAGCTTCTATAACTT CGGGGTGCGATAAGAACATGAATACAGATACACGGATTGCAACAGTACCCA AGCCACTTGTTTTAAACAAATAACAGGATAATGGGGAGTAATGTAAGCTATT GACTGGGTTACAATCAGGGGTCTGATAACAATCAAACATTGTCCAGTTGCCTT TTGCGAATATCAATGACCACTCACGAGTTGCAACTGATAACGATTATCGCCG CACAATGCAGTGGGTATTTCACTGGGGGGAACTTTTGGGTCCCTAGAA CCCAGACGGATTACTCAATGAATATAGGCGATATGTTTGGGTTTACAGCGAA AGTGCTATTAATGTCGACCGTATGCTCTCTTCGATGTGCCAGCTCTCTATTTGC GGGAATGAATGACTATTTTATGGGTCTGCCGTCGCTGCTACAATGCTGCATT GCTGCAGTGGGACATCCTTTGAACAGGCGCCATGCCAAAGGATATTCTTTGT GGAAGGGGGGGGGGCAAGGGTTAAGGGTCACATTCGTTTGCGCAATAC TTCCAGCGATGGGCGGTGAACGGTGGGCGGGCGATCGGTCAAGGCTTCGA CTGTGGAACGTGACACGCATATGTCGGCCGGAGTTTGGCCCAAAAAGTGGCC CCAATGGTTGTCCTTCGCGCTGGCAATTAGTCCCTAGCAAGGCGCGTCCATAT TTTGCAAAAATTCGTGGGGCGCCTTGTTTTCTTCTCTCTGTATGTGTGCATGTG CGGTATACGGCTGCGTTTGTGTGTGAGTGTGGGTTTCGGCTCTACTCTCCCGA TGATCCTGCTCCTGGTCCTAATCCCGGCCTGCTCGGCTGCTCCTGCGTCCT GACTGCGCTAGAAATTCGCTTAAAACGAGCCTCGACGGGTCATTTTTACAATT GTTTTTGTTGTTCCGTTCGGCTGTTTTACCAGACGTGCTCGTTCCGGTGTGAC TGCCCGCCGCTGACTGTAAAATACTAAACGCATTGCAGCTGTGGCAATGCCC CTTTCAGTTACTTTTCGTTGGCTTGAATATTACACTAAGAATTCAATTTGACAC TTGCAATTTATACATTGTATATTATAATATATATATGTATTATATTTTATATC ATATAAAGATATTTATATCTATTGATCTTTTGATTATAAGCTCTTTGGTTGAAC AATATAAGTGCAACTTTCTCCATCACCTTCCTATCTTTTTACAATATGCTTACC TCGTCAATACGTTTTTCTATTTCAAATATTTCAATATTTCAAAGAAATATTTT GTTTATTTTTCTGTGTGTTTTTAAGCAATCTGACCCCTGTAGAAGAATCCCTTA TAATATTAACAAATGTATCCTCAAAATAGATCGATCTCTATCTTCGCAGACTT ACACGAAACATTCCAGAACCGATAGTTTTATGCGATATATGAGATTTAAGGA GTACTTTCCGCATTTCGCCATCACAGTCACGCTTTCCTTGGCATTTGCAATCA AATAAGCGCTAATAATAATCGTAAAAGCATAAGAAGCATATAAAGAAGAGT CACCGCCAAAAGCATGCACAAATATATATAAATGGGGAGCGATTTAAAAACA

#### FIGURE 17

dTPR2 5' region, 13015 base pairs

AGACAAAGACAGCGCTGACTTCAGTCGACTTTCGTATTCATTGTTAAATGACA TGCAAATGTACGAATGACATGGCATTCGCCAAAGGGTTTTGAAAGGGGGGCC AGATCCAAAGGGCAGGTCTCAGGGAAATGTTTCCAGGCTAATTGTGGGTTTT ACGCCCTGTACTTCTCCAAATGATCAAGTACGTCATTTAATGGAAGCCACTGA ATGTAGGCTAATATTAGATTTCTGCGCTGAATTAAAATTATTGTAATACGTAT TATAATGCATTTGTACCCAAATTTGACAGACTTAAGCAGTTCTCTAACATAAT TGGCATCATTGGCAAAGAGAAATAATATTAAATTGGCAGCATTGCCAGAAAA AACTCTTCTCCTAAATTTTGCTTGATTGAATGTTGTAGTTGAGAATGTTGTAA AATAGTGTTAGTATTGTAACACACGACATTTTTCAAATATTTAAATGAAAATC ACATGGTAATTAGCAATTTTGGGTGGCCTTCTTTCCTCCCAAGCCAAGCCA TATAATTTCAGCCAGCTACTTGCGATTTCCCCCATGACCAACAACAACAGCCC CATATGTGCAGTGCATTAATGCAGATTTCTTGGCAATTGTTTTTGCATACTTTG TTTTTTCCTCACTCACTTCAATTTCAATTGGCGTGCTAATAACTCATTTAGTTC GCAACAAAAAACAAAAACGAACAGCGGGCCACAAAAAATGTAGCTACAA ACATGGCACAACAATGGATTGGATGGCTAACCAAGATCGCCCCCACTTC CCTTTCCATCAATTGCGAATATATCGCATCTCATGATGCTGAGAGAATACTCG TACTCAACTATGCCGACTTTATATGAACACTGTGTGCAGTTTTGTTTTAGGCTT TGTAATTATAAAAAATAAATTGAACTATTGTTGCCTCATTTAGATTGAACA GTGAGGCAGCCACAATGTTGCTTTTGTTATTCGGATACACTCAATTAAGCTGA ATTTGCAAAATGCAAATGGCCCGTATGAAACTCACACCTCGAAAATCATAGA TCATTTTGACAGCCCGAGGAGTTCGGTTGGTTCAGTTGATCTCTTGATTGTCA GTCAGTCATTTGTGATTAGACATTCGACAGTCGCCGCTATTGTTGGATGGCAT AAATTATAGTCTGTCTCAACAACAAGCGCTGCATATGAAATCCACATAATA AATCAATGTGCTGTCGTAATTTGTGTTAAGTTATTTGTAATCAATTTGAATTCT CGCCGTACCTCCCACCCCCTCGGTTGGTGAGATTTATGGGAATATTTTATT CATTTTGCTATTTTGGTTAAATGGCTTTTTGGGGTTTTCCCGAATATAAGTTTA AAATTAACGCGGCAATAGGCTTAAGATCATGTAATATTATATTGCCCGTA AACAAATGCTTTCTACTTTCATTATCATGAGTGTTTTAAAACTCCACGACTGC TCTAAACTTTAATCTTTAAATATTTTTGTACCCTTTGAAGAACTAACCACTTAG CAAATCCCTCCTATTATTTCCTCAAACTCTTGCACTTATCGAACTCGCTTCCTT TCCCGCCATCTTCACTCGAACAAATTTAACAACAAATTAAACTGAAATGCA GTCAAATCAATCGCTGACTTTTCAATTCGTTTTTCCTTCTTTTTCGGCCCAACA TTTTCCACTTGGCCCGAGCGTTTTGCATAGTCCATGGCTTCGATTGGATCGGC TCGGATCGGTTGGTAAGTCTTCGGCGGAGTATGGCTTTAGTCCAATTTAGTGG AAAGGTGTGCCCACCAGCTCGGTCACAACACGTTGCTGTGGCTCATTGGAGT TTCGCCTTTGCCTCGCTGGCTTTTGAGCCGTTTGGTCGGTGCCGCTTAAACGC CGTTTTAGCCAAGTTAGGTGAAAAATGCCAAGGGAGTGAGGAGTGGAGACC GAACTGTCAACTGTGATCAAAATCAATTGTTTGCCATTTGCCAAACCAAATTG ACTGAGCCAAGTCAGTGCGAGTCACACAAAAATGCTGACAAAATTATACCAT AACCCATGAAATGTCAGTGTCAATAATTTTTGTAATTATGAGAGCATTGAGCT TGAGTACATAAAAAAAGTTATATATATTAAAAAAATCATTATTTTAGTTGGC

TGCCATTGGAGAAGCCCCCAAAAAAGGCAAACAAATATAATAAAAAATTATT GCAACGTAAGTTTTGATTTGAACAAAAGGCGTATACAATTGGATGAGCTCAA GGTTCGTCTCTAACATTTTCAAAAAAATTACATAACTTTTAAATTTGATTTCA GTTTATTTGTAAGTGAGAAGCCTATTTTCTAACCATAAATTCTGCACGTTAAG AGTATTTCCTTTCATATCGTATCTACAAAAATCAATCCAACACACCTGTTTCA TCTACCGTTAACACCGTTAAGCCCCGCCCCATTTTCTTATCGAAAATATAGCC AGCTGGCATATCCTTTCGACTTCCGCCATTCGAGGCTCGCCCAATTTCCGTTT CGAGTTTAATTAATTAATAAACAAATTCTTTTCGCTCTAAAAACTCTCAAGT AAAAAAAAAACCAAAAAGTAGGAGGAGAAAAGTTATTGCCATAGTTTTTTT ATTATACTTGTGTTTTACCTTTCTGGTGGCTTGATCGATAGGCATCTGCAATT AAAAAGAGAAGAAGAGACAAGTGAGGCAAAATTGTTAAACGTTTTGTG CTTAAATTCGGGGCACAAATGCTGAAAGGGAAGTTTTTCATTGACGGGTTCG TTCTGACGGACTTGCATTTTGGCGGGCAAGCGGGTGTGAAAATGCACACGCC CCGAGAACCCCCTTTCCACCCCCCTGGACCCCTTTATCCAGCCCACTGGCC AAAAACAATTTGTAATTATCCACAGAGAGCGCTGCCTTCAGCGGTTTCGCATT TCCCCTTTCGCTCGCTCTCCCAACTTGTTTCAATTTAGCGCAAAACTTTTTCAA CCTAATAATAGGTTTAACCGCATTTTTAACCGTTCCTCATGTTCGGTCCGGTTC GGTTTTCAAAACCGGGAATCGTACTTAGACTGGGTCTCCTTATTTCTGTTCTG GCTCTCTGTACAACTTTTCATTGAGAAAAATGTAACTAGTTTTTCATAGCAAC GGAATACAATTTAATCCAATAATCCAATAGTTTAATCCAATACAAATGATATT ACTACCATTTCTATTTTCGTTAATTTCGATTTGACTTATTTGGCTGGATTTACT TTTCAAAATATATGTTATCAATAAGACACAAACCTTACTTTCTAGCTATTAA CATAGTTTAAAAAAAAAAAAAAACTAATAAAAATTACGTGAATCTAAATTTT TAAACCCGATATCCAAGAAGATCTCAATTTTTGCCTGTGTACTCAGTTCTCTG AACAAAGCGCATGTGCACTTTGGAGCACACTCCATACATGTGGCTCAGCCCT TTTCCATAATTAACTAGATGGTTTTCCATCGACTTCATTGTGGTCAGCGGCCA GTTCAACCGTTCTTCACTGCAACCGAGAACTGTAAACACAAAAACCCCAGG AAGAAGGGATATTGAAATACAAGGTTGTAATCGTTTCGACTGTTGATGTCTC ATGTTTAAATATCCATGAAATATTTGGATCTCCTGGGGATCAATCGGAATATT AGCCTTTAATTGTGTTGATCTTTTAAGCCTTTTTGTATCTAATCTAAGCCATTC GATCTAATCACAATTTATAAATATCTGCATATTTCTGTATAAGTCTGCATCAT TTGACGTAACTCTTTAAGTCTTTTGGCTTAAGTTGCAACTATAAGGAAGTATT TATTTTAGAGACACAAATATTTCAGTCGCCTTCATTTGAACAAATCGGCGAAA ATTGGCTAGCTCGCCAAACTTTCTGTAACCAAGGACAATGGTTTTATTTTAAA CCATTAAAAACTTTAGACCCACTAGCTCCTAGATCCCCCTCAAAAGATTTAAA AAAAAAAAAACACGATACCCATTTCTACTGAACTTCGTTTTTGCTTGTCGTTTT TTCCACTCGAACGGAAATGAGCTGACAGCGCACCGCACACGTCGATTGCAGA AAAACATCGGATAAAACAGGAGGAAAAGTTGTGCAAGGTGGAAAACTGTTT GCAAGGGGTCACCGGGGAGCGTTACGTTTGCATTGCGTATTTCCGCTAAATGT



CATCGGAAAAGGCAAACGCGAAATGCGAAACGAAAGTTTTTTGATTGCCCG TGTTAATCGATATCGATGCACAAACTATTTGCATTGCAACCGTTGCAAGAATA TGCAAGAAGTTGGGGGCGGCCGCGCAGGGGGTGGAAGTTGAGTGCGTAAG TTGGCTAAAGCGGAAACAGGAAATGAGAAAATTTTGCAGAGCAAACCCCGA ACTGGAAATGCAACTAACTGGGCACATGCACTTTGCGAAATCATTGGATAGC GTTAAGAAATTTATTTTAAAATTGTAACTAACATTTAATCGTATTCAAAAGCA ATTAAATCCCAATCCAATTCTTATATAAAATCCTTACAAGATTATTCTATTTA CTGTAAATCTAAGCAAAAACTCCCTTTGCAAAATATTCGCCTGCACAGCACA GATCAGTGAAATAATCAAATGAAGTCTTGAAATAACGAAAAACCCCCAATTG CGTGTGGAACTGCCCCAATGCTTTTGCTTCGGTTTCGTACCTGGCCGTGGTG CAGTCCCTGTAGAGGATGTCGAAGTCCTTGCAGCAGAGCAACTTGCAGCGAT TGACGCCCGGCTGGATGGCGCCCAAGCCGCGTAATATGCGCACCTGTTCCAC ATTGCAGACGAGCGGTACGATGTCAAGGCGCTTTAGTTTGGTATAAACCGTA TGCAGACCGCCGACCAAGTGCTTCAGGAAGAGCTCGAAGGCCTGCGGCAGGC AGAGCATCGTTCGTTGCTAATTATGAATGCGGCGACCTTCTGACCCCGGTAC TCCACCAGCTTGCACTCATTGGCACTGGGATCCGAGGTGGAGATCGGCGGCG GTGAGTTGTACGACCTTGGCGGCACATGGTGATGGGCGGCGGCCATCAGTTC CAAGGGGGAGCATGGTGCATCATCTGCAGGGAGTTGAGGAGCCCCAGCGA ATGGGGCGCAGTCCATGGGGCATTCTGGGCGGTAGGCCCGTCGGCAGTCCG TTGCCGATGGCATTCCATGTGGCGGGGGGCTGAGCTGATGGTGTTGCTGCTG CTGCTGTTGCTGCTGTTGTTGCTGCTGCTGCATCTGCATCATGGA GTGGTTGAGGGAGCTCACCGGACTGACGGCACTGGGATGGCGACTTGGTGAA CTGGCCGGTGAGCAACTGGATCCTCGTCCTGTGTGCGAGCTCCGTCCATTTGG ACGATCCTCGTTGGCTCCACGCGAACTGTTGCTACCGTCGCGTCCATTGTGCT TGCTGCTGGTGATGCATCAACATGGCGGTGGTGTTCATATTGCCCGCGGCTCT TTCAATACCACTATTAATATTGTTATTTATTGCGCCCGCTTTATTGTTGTTATT TTCACTCTGTTCACTTGTCACAGAATCCATACTTCATCATGGCCGACACTTTTG TTTATTTACTTTTAATCGATTCGTTAATTTGACGTTTTTTCTATCGTGACAAA AATTTGACACAAAGTAAGGGAGAAATAGAAAATAGATGGTGAGAGGAAGAT AAATAATTAATGAACTCTTAATTCATTTTTAATTATTATTAGGCTTCTATATG CAAATTCTAAGTGAGCGTGTCTCGTATATTCCTATCCGCTTATTATTGGCTTTA CATTTTAATACTTCTGTAAGTTTTATAACATCAAATTTAAATGCAGACCTTC AAAAAATTTACAAACGATTTAGGATTTGTATTAGGCTCAGCTATGCTCCTATT TATTAAAATCTATTTTGAGCCAGTTTAGTTAGTTATATGGTAGCTACAAGTT AAGAAATATAGAGAACTAACAGAAAATAGAAAAGTTTCCTTTCAGACATTTA AAGTCCGATTATCTTCTAATACCCCCCATAAATAATCCTTTATCAACAGAACT ATTGCTTTGCAAACTTTGCTTTAATTAAGTTTTGGGAAAAACAAGGCAATGAA GCTAATTTGGATCCTTACTGCCAATTTGCATAAATATACCTATTGTCAGCTTT ATTTGAATAATTCGATATAGAACATAGATTTACCTTTAAGGAGGTCTAAAAGT AATTTATAAACTCAACATCACTGACACAAGACACTCGCGCACTTTGCTTTTTG CCGCTTGTGTTAATCGAGTTCGAATAACCGTTTTCGTACTGGAATTTTGGAAA CCGGAGCTGTCCGTTTTCGAGTACCGTACCGACGGATTGTCACTCAGAGAT TGAGAGATGGCAGCTACTCCGCTGCGACGGCGACGGTGGCGTCGCTCT



GCTTCTTCGCCTTCGACTGGTTCCTCTTCCCCCTCTCGTTCGGAGAAATCAAC GAAACGAATTGCATTCGAATGGGAATCGACTGAGAGCGAGACGGCGCGAGG CGACGACTGCGAGTGAGCGAGTGAGCGGGCGCTAACGAGTGCTATTTTTTA GCCCACCCACACACACGTACGTACGTACGTACACACGAAGCGCTACCGTTAT GTACTGAGAGAAATGCGCGCGCAAAAGTTTTATTGCATTACCTTCTCTTGCGA ATGACAAATTCGTAATGAAAGGCGAGTTTCAATTCGATTCCTTTCGGATTTTC GTGGCAGCGACGCCGCAGCGCGGTCGGCCGAGACGAGTGTGCTTGTATGTG TGTGTCTGTGCCTGTGAGAGCGAGCTGGTGTATCTGTATCTGCGATTGTGCAA AACCAGAATACGAATACGAATACGAATGTCTGTTGCCCGTCCACGT CTCGCATTACACCAATACCAGGCCAAAAAGGGGAGTGGTATGTGCGATTGAT CGGTGTGTTTGCATCTGTGTATATTTCTGTGTGCAACCCCGAAAATACAATGA ATCTCGCCATCTCTGTCGCACGCTCAGGTGGGCTGCAACCAATAAACACGAG CGAGCGAGAAAGCAGCATATTTGCATAGCCAGTCGTACATGTTTGCGCTCTC GCTCGCCCCATGGGCGACGCCTTATATAAACAAATGACAATTGTTTTGGCAT TTTGTGTTGCAAAGTAAATTATAATAAATGCATTGCCAGAGAAGAAAAGTAA AAAAAAATAGCTTTACTTCGAGTTTGCGCAGCTGTCTTTGACAAAAAGCATTT TAATTTCAATTAAAAGTAAATGACAAACTTTCAACGAATTATACTTTTCGGGG CCGTTTCCCATTCGATTCGAGTCCCGTTTATTTGTATTTCTTTTTGTGTT CTTATAAATAGCATTGCTTATAAATTCTGGCATCGCACCTTTGCCACCTCTAT ATGTTTATGTACAATGTATCTGAGAGCTCGGTCATTTTTCTATTATTTGTCTTC GTTTCGCCTTCTGCGATTCTTCTCCATAACGATTGCCATTCCGTCGCCGAACC TGGGAATGGAATACGTCTTTATGTATTGTGTTTTGCACATGACGTATGAATTTT TCTTGTTCGTTTCGTGTGGGCTTTTCTTTTGTGGATTTCCTCACCCACTGTCTT TTAGGTGACAGCAACCATTTAATATTAAATTGATTGCAAATGTGGATTTCCAA CAGCTTTTAGAAAATATTTTCGGGCTTTAAAGAAGAATTTAAAACACAATAA TTATAAGATTATATGAAAATTAATATGTAACGCTACTTTTTTCTA AACTGTGACATTTTAGGCTATTTTTTTTTTTTACCATTTCCTTATGTCATATGAA TTTCATTTAATTATGACATATACATGAATCGCTGGCTTTAAATTCGAATAAGT AAATTTGTTTTCCCCCCATAAATGGACAACAAAAAGGTACTGCCTCTATCATC CAAGTGTCAAAATATGTCATAGCAACCAACTATCGTCAGTAAGAAATGAGTT CTACAACATGCAACTTTTTCATGGTGTCGCAACTGTGGGCGGGAAGTTTGATT TTTCGCAACAACAGCTCGCTTTGAACTCTGGTTTTTCTCTTTAATAAATGCA AAAGATGAGTTTATATTCTAAAAAAAAGGAGGGTGATTAATTTCTATTAGTTT GGATTACAAATTTGGACTAGGAGTCAATTTGAAAGTCGTTATATCAATAATA CTTCTGGACTTTGAAGCGACAGTTACTGTTCCATAACTTCGGATTATCAGCTT TGCCTTCACCACATATATAGAGTATTCTCTGGATGTGTCGAGATTTGTATTTTT

AAACGACGACTGGATGGCAAAAGTTCAGTGCGCTCGCAGCTATTATGTGGAT TATCTGCCTCTTGCTGGTGCCCCTTGTGGCGGCCAGTTCCAATACAAGACTTC TAAATGGCATCCTAAGTCATGTGGACAAGGAAGCCAATCCCTGTGAGAACTA CTACAACCACGCCTGCGGCCAGTACAACATGCGTCACATCGACGACACCTTC TTCGACATTATACAAATGCTGGATCACCAGGTTAACCAGAACTTGGTGAAAC TAATGGACGAGCTGGAAATGAGTTCTCAATTGCCGGACTTTAATGTATCTAGT GTAGATGCCAAGGTCCTTCGTTACTACCTTAGTTGTCGTGGAGCGCCGCGGA ATATGGATAGTTTAAGCCAGTATCTGAAAGTGATTTCCCCCGGCGAAGGACT CACATGGCCTCAATTCATTCCGGACGGTAGTTCTTGGCCCCAGGAGAATTTCA TTTAACCTTGAAGTCGTGTCAAACCCACGAAATGCCAGCGAGTACATGGTAG AATTAAATACACCCACTTTTGGAGAAGAATCTCAACTGCCGAACAGTTTTATT GAAATTCTATCCGTTCTCTATATCATAAAGGTTCCTTCCAGTGAAATCATTAC TCTGGCGCGAAAAATGCGAACGCTTGAATTGTTGCTTAAAACGATGATCAAT CCGATCGACACACTGAATAATAGATACATTAGTATCCGCGATTTTCAGATGG AAACCGGTCACAACTGGCAGCGTTTCTTTGAGATTTTAATAGGCTCCAGCGCA GCCCAGAACTCCAAGTGTTGGTGCGCAATTTTAGGTACTTTACCGCCCTTAA GGAACTAATGGACAAACAGGATGCTCGGCTGGTGGCCAGCTACATAATGACC CGATTTGCAATATTTCTATTGGATGAAACCATGGGTGGCAGAGAATCCACGG AGTGTGTGTCACAGGTGCGCCGCAACATGAATTTGGCTGCAAACATGCTCTA TAAGGAACGATTTTTCGAAGACTCCACTTTCAGTGCCAATATCCTGGAAATTA AGGACATTTTCGAGAAACTACGCCATCAGTTTCTGCTGCAAGTCGATCAAAA CAATTGAGATCAACGTTGTGAATCTTCCAAAAACCGATGATCTTCGCCATTTC ATCGGCCAGTACTACCAAGACTTGCAGTTTCCCACTGGCGAGCTGGATTACC ATCAGGAGCACCTCAAGGTGCTGCAGTTTCGCACCCAAAAGATGTTGGCCCA ATCCAGCAAAGGGCACTCAGAGGAGCAGAATATTTTGACTTACAGGAGCCAA GCGCCCCTCCCCCCCTCGTACTATGTGATGCCCCCCAATGTGATTATT GTCCCCTTGGGCTACTGCAAGAGCCATTCTTTCAGCTGGAAAGCGAAGATG TCTTCAAATACAGCCTGATGGGATATATTATGGCACATCACTTGATAAGCGCC GATCGCATCGTTTCGAAGAAGCAGTCAGTTGCTTGTCACGCAATTCAGAGAA CATCGATGAAAGCATGGCCGATATTGCTGGTTTAGAACTGGCCTATTTTACTT ATGCTAAGATGGCCAAGAATCGAAACCGTTTGGATTTCACCCATTTGCCACC GGAGCAGATATTCTTCCTAAATGTTGGCCAGTTCTTCTGCGGCAATAGCGATA TGTTGGTTCAGTACAAGGAAGATCAAGTGCGTTTACAGCGAGCTATTGAAGG GTTTGAGCCATTTGACAAGGCTTTTGGGTGCTACCGCAATAAGCCTAAGCAC GAGAAGTGTCGTTTATAGTGAATACCTTGTACATATGCTTAGAAATACATATT TTTTGATAACAATAATACAAGACAATCGTGTTAAATTATAAAAGTGTTACAAT CACATCCATTCTGTTCTTTTAAAATTAGTTTTAAACTAACAATAGTCAATAGG CTAAGATAGTTAAATGATCATCATCGAATAAACAACGTTCAAGATTGACTCT AAAGTTATACGTGTGTTACTTACATGCATTACATTCGGGCCTGGCCATCCACT TAATATACTGAGATGTAGCGGTCTTTGATTTGCGGGATCTCTTATGGATTTTA GAACATTGTTAACTTTGCTGACAAAGTAAATTCAACTTTTAACGACTTGTGGT GTGTGCGGCCCGATGAAATGTCTTAAAATACAAATTAAATACAATTCAAATA

TAATTCAGACGTCAAAAGGTTTAAAGTTAAAATATATTTTACCTTTTAGTGTT ATTTATACGTATGAGCCTTGAAAACACAGTTGAATATCAAACGGATTTTTGTT ACCAACAGATTCCAACAGATTCTCCAACTTTCGTTTTTTGATTGCCTATTCACT CGAAGATCTATTTCCAGTACTATGATCCTCCATAGTAGAGTCAGCTCAGGATC TTGTGATAATCCGCAAGCAATTCGACAAAGAATTCGTCGGCCAGAACAAAAT TTATTAAATCATTGTAGTCATTCTCAGGATCTCTCTAACTGGCAATCCGTAA TAACGTATTTCATTATCTCCAAAATACAGTCGGAATTCAGATTAAATTTGCCG TTTCCGTCCTTTTTTATAAATATACATACAAATATACTAAGCAATAGACTGAA ATGAATTCTAGAATTTGAGGAAACTAATTATGTACCTTTATGAATACTTTTCC TTACTTGTACTAATCAAACTAATTTTTAACAGATTTTTCATGCCGAATGATTA CAATCTTATTTGGATGATTTGATAGAGCTTAGGAATAATGGTTTTAATTTTGG ATTAAAGAGTTGCGATTAAGAAACGAAGATATTATCTAGTTTTTGAAGAACA CAGGGTACTTTAAATTTCGCACGCGGAACGTCAAAACAAGAAGAAGTTTTCA TCAACACTGAATTTCCGCTTGGTAATCAGCTGATAAGCGTGCTCACGATAGCC GAGTTCACATCCAACAGATGTTTCCCTTAGCAGGGTTTCAGACCCAAATGATG ATTTATCTTATTTTGATTAAGCTCCAACACGCATTGCTTTGCATAATTCAGGTA TTATTAGGCTGCTTAATATACAATCCACTTATATTGTTGTCCATGAGGAAC ATCGACACGTGAGGATAAAAATATTTATTTATCGATATATTTTTACTCTTGAG CCTTTTGCACACCCCTAGTTGTGTTCCA

#### FIGURE 18

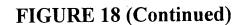
dMLF 5' region, 8374 base pairs

GCCTGATTGTTTCCACTTTGCAGCAGAGGAGCCGGGAAGGAGCGGTAGAGG CGCACCCAGTGTATCCGGCAAAGGCAAGTCACCCCAGGTGCGTTCCATGCCC AGCTCTCCGCTGCCTCAGCGATCCGCTACGCCGACGCGGCTGATGAGCCAAC GTGTCCGTGAGGCGGCCGAGCGTCTTGCCCAACAGCACACGGTGGCCAGTGC TCAGCGGCATTTGGGCAATGGGAGAGGCACTGGCACTGGCAATGGAAATGGC AATAGCAATAGTAATGGCAATGGTAATGGGAACACCGCGGAGACGAATCGC GAATCACGCGCGCGACGTCTCATCAACCGATTCAATAGCGAAACGCAGCATA TCACGTCCTAGTTTAAGTCGGTTAAATGCCGACGAGCATAACTTTATTACAGA AAACTTTACGAAACACTCGAATATGAATGCGACTGCGGATCAGCATCCCACC GCATTCAAGCGGATGCACTCCCTCCGTTCAGAGGGAACTGTACTTAGGCTAG AGGAAGCTAAGTGTTTAAATTATTGTATCGATTTATATACATATTTACCATAC TAATTAAAGTTAATGTAACGAAAACGCAGGATCAGTAATCTTATTTAGTTCA ATGGTAATCAATGTGCGATTAGCGGATGATCGCGCTCCTTGAGTCGCACCCA CAGTCCGCCGGAGGCTCTCAGCGTAATCCGGAAGGTGGCCGCAATGGTTGTC TTTCCGGTTACAGGAAGCAGCTGGTAGCTACGCAGCAGCGCGACACTATGG TCTTGATCTCCATGATGGCGAATCGATTGCCAATGCAATATCTCGGTCCAGCG CTGAAGGGTAAAAAGGCGTAGGGATGACGGTTCTCGGAGTTCTCGGGCGAAA ATCGCTCCGGCTGGAACTTTTCCGGATCGGGATAAATGTGGGCAAGACGATG GGTGGCATAGGGCAAATGAAAACGTTGCTGCCGGCGGCCAATGTGTGCTTT GCCAGGCGAACCTCTTCGCCCAGTTTACGAGCAATAAGCGGGACACTGGGAT ACAGACGCAGTGCCTCCTTGATGCACATCTCCATGTAACGCATCTCGTGCAGA TCCGTCATCGTGGGAGCTCTATTACTGTCCTCGAATATGGTCGCCAGCTCCAG GACACAGCGATCCTGGCACTCGGGATTCTGTGTCAGCAGAAAGAGAGTGAAA GCCACGGCGCACCCACCGAATCCTGGCCAGCCAGCATAAAGGTACAGGCCT CGTTGACGATATCCTCCTCGGTGAAGTCCCGATTGCTCTCGGAGATCTCGATC ATGTGGTCGAGCAGACACTTTCGCTCGCTATTGCCATTATTATTGTTCTGGAT TTGGCGACGTCTCTGGATCATTTTGCGTGTGAAGTCATTGAGGCGCTTCTTCT GGTTAAGCTCATCGTTGGCCATCTTGGTCCAGTGGTAGATCCCGTCCAGCAGC AGCCAGGGTTGCGTAAACCGCGCGGGCATCATGATCTTGCCCTGGCGGAACG GCGAGTCCTCCATCATGGCCACATCCTGACCTCTTTTCTTGATCGGCACACCC AAAACGGCCTCTGCAAGTCGTTCAGGGATTAAGTGAGAAATTATAGCTTGCT AATCCCCTAGAGACTCACCATTTAGTATGTCCAGTACACAGTTGTTCACGTAC TTGGCAATATTTATCTCCGTTCCCACGGCTTCGGCATCCAGATTCTCGTACAA CGATTGCGAGGCATCCACAAAGGTGTCGATGAACTTCTCCAGCAGATTGTGA TGAAACGCTGGCTGGATGAGCCGTCGATGATTGCTCCACTTGGAACCACTGC TGGTTATCAGCCCATCACCCAGGAAATTGTGCATCAGTCGGTAGAAGAAGAC CTTGTTGGTGTCTTCTCGAGGAGAGTATCACCTGCAGATCCTCCGGCTCCA GGACAGCAAAGAAGGGAAAGAGCAGCACCCAGATCCGCACCAGAGATCCAT ATAGATCGAAGGCCTTGCCGCACATCTGCGCATCACTGTGAAATGGGATTC AATTTAACTTAAAAGGTATCTTTCACGAAAAGGTTTCTTCAAGGATCTTACAG

TCCTTATCCGTGACCAGCATGCAGTTGCCCAGAAATGGCAGCGATGGCGGAC CCGTGAGTCTCAGCGAGAGGAGAACCGATCTCAAGTACGTGTTCAGGGTGGC GTAGAATGTGTAGATGCTCAGGCTGATCACCAGGAGGATCAGAATGGAGCAT AGCTCCAAATTGGTGGTGCGCTCCAGCTGTGGGGGCGAAAGCAAACGTAAAT GCATTGGGTCAAGTCGCGTGGATAATTGCCCGCTTAGGTCAATATTTGGTTTG CTATCGAGAACGCCGAGCTCTTGAACGCACTTCATCAGCTACGCACTGCGCTC ACTGGAGTCTAATTAACTGAGGAATCTTGGAGCACTTAGGCATTCGAACTTG GATGCGAGCACTTGCCCTTGCCGCGTGTCGCAAGTTTTCGGCAAACACACGTT ATCGTAATCGCAACGAAAGTATAAGTTATGTATCTAACTGCGGTGTGAATTG ATAAGATCGATTAAAGCACCACACCGTTCATGTGTACGTGTTGCTTTG GTTTTTTTTTTTTTTTGGGCCATTCGCGTCGATGTTTCGTGGTGCAACAG GTTACACGATGAGCACAAAACATGACAAATGATGATGATCACCGGACAAAA ATCCAGGGACAGCCTTTTGTTGCCCACACTTCCCACACCTGTCGTCGCCCCAC GTTCTGGACGAGAGTGAGAGCCCCAACACCATTAGCCAAATGCGATTGGTTT CAGGGCCAAGTGAAACCACCGGTTGGTTAACTGACTCAGATCTCAATGATTA ATTTATTACGGACAAGGAATCGGCAAACGATCGCAGTTGGTCATCATAAAGT TTATCCAAAAATCTAGGTGGCATTCCATTTAGTGGGAACTTCTTACCATCAGT TCGTAGTAAGCTAAGTTAAAGAGTAAAATAATAGGCGCTTTTAATCCTCCTCA GCCACCTCATCCTCGTAGCCCTCGGGCAGGGCATTCACCTCGGCATTGTGAAA CAAACTGCGATTGCCATCTCCCCATGGGAATCGTTTGGTCCGCCGCCTCAGGT ACTCGTACTTGGCGAACGCTCCCGCTCCACGTGCTTGTGTCCGGTGAAGGCG TTTGCGGCGCACAGGACGATGGCCGGTAGGGCCAGCAGGAAGGTGACACGC TTCCACAGACCAGCGGTATTGGCGGGCATATTGCCCATAAGCCGGATATCAA GGCTAAGCTAGCTTGAATTTGAATACTACGTACTGTAGCGATTTGAATCTGAT CCGTAACACCCACGCCTGCTGCCCGAAACTATTGTCGCAATTAGGAACTCTCA AGGGGATCCGAGCCAGCGCCACAAGGTCCAACAACCCGCGTATCTTTGTTTA ATCAGCCCAATATTTGACCAGAAACCGCTGAAGCGTCCAGAAGGCTTGCGCT CTGCGAGGTGTGCAGAACCCGCGCGCGTGTTTGCTCGCCAATTGGCACCTGGC CACTAATAGATATACATCATGATTATTTCCCACTAATTCCATAAGTTATCATA ATGGTCTTCCTAAACGAGAGGCTGCTTGTCGAGGCACTAAGACCGCCCAAAA TCTAACGATCCATTGAGATTGCGGTTAAAAATGATTCAAATGCAAGCGAAGT TACTAAAATTTGTGAGAGTATATCTAGTTGAAAACTTGAACTTGAAAATGTG GTTTTCATAAAATTATCCAAATTGATGGGTGTGAATTAAAATTAAAATAAAAA GATTAAATAAGTTATAAACCTAGATCATTTCACTTTAGTATTGGTAATGA AATTTAGGTTTATATATCCTCACTCTTCTTAAAGTAATGTAAATATTTGTTATC CTTTAGGAAATACACCTTATTAAAATAATTATTTTAAATTCTATTAAAATTCTT TTAAAAAACAGAAACGTAATAGCCACCATTTTACATTTTACTTAAACGTTTTT CCTTTTCTTTTTAAACTTTAGCTGTGAGTAATCCTTTTTATTCATAACGAATT GCGTTTAAATATTTTTATATTTTCTTCACTCACCACTTTTTCCACAAACATTTT AGTCACGTATTTGTATTCCCTTGATATAGTCAATATATTTTGTTTTATCTTTA



ATAGCTTCACACAAAAGTCCTTGCCACAAGCACTGTCCAAATCCACACATAC ACCAAGTTAGTTAGCTCCACTTCGATTTGGGATATATCCGTATTGTGATCTTA TTGGCCAGAGTCACATCCGGCGACTGATGAGCTACGAGTGCGGGACCTCCGC CGGTTAGCGTCTATTTATAACCGATTTGGCCCGATCAAGCTCGGCTTGAACGC CGCCGAAAATGATGTACGTGCTAGCTAAGTCGTTGGAGTCCCCGGATACCCG AATCCCCGTATCACCGAATCACCAAATCGCCGAGTCGCCGCGTATCCGCTAG ATGCCCGAGTGTATCGAGTATAGGTAGTAATTGCCAACTAGTCGGCACTCGA AGTGCTAAGTAGCTAGAAGTGGATATGGTGCTGGATGCTGGATGCCCCTGCC AAGTGGCATGGCAATCAATTATCCGTTTGGTGCTTGTTTGATGTATCCCTCCT CCGCCACCGCCACGCTATCCACCTCCTCCATGGAATGGCAGACCCTTTGGGT TGCCAGTGGCACTCAACGATCTGAGCGGTGGGAACGAGGGGGAAGTCAGCT AGAAATCTTCAGACGCGTGCCAGTGGATCGAACTTTGAGCGGATATTCAAAT GTGTAGTCGTCGGATCTTTGCACATTCACATACTGTTGCTTTTAACGTCATCAT AAATTCTACAAAATATATTCGGGATTTATTTCCGCGAAATTTTAACCTTTGCT ATCATTCAGTATTCCTAGATGTGTTTAGTCAGTTAAGATCGTTTGAGTTATAG GTTTAGAAATCTTGGAAATTCAATAGCGCATTGGTTACTGATTAAGAGTTATT ATCAGTAAGAATATTATTAGTAATTATTATTATGCCAATCAGACCGATTAGAC TACCACTTCTTGTACTTTTGCTGCGAGTTCTCGTGCACCACCGATTAATATGGT AAATAAATCTCAGCCTGCTTTTCCAACACCACTTATCTGAAGACACGATTCCA TGGAGCACATGGAGATTGAGATTACAGCCATCGACTAGACGCCTTCGTCATT CGGATCGCTTTGCTGATAATCCCCATTTGTGTTCTCCTTAGCTGGCCAGTTGA CTTTTTGGTCAGTTGACTTTCTGGCCAGTTGGCTTTCTGGCCATTTGGGTCTTT AGAAGACCACCGCCCAGTTTATAATGGATATAAAACGAATTGAGCTGCAAGT CGTATAAACTTTACGATATCATAGCAGAAGTTTATGAAAAATCCAAAATACCA ATCATGGATGATCGCTAAATTCGCCATTTTGGTGATAAGTGATAAGCTGGCTA CTCCAGCCCTATATAAGAGACCTAAATCGAACCACACTTTAAGTTTAACCATG TCGCTACGTTTGGGTTTGTTTCTTTTGGCTGCACTTGGTGTGGTAATTCTCACG GATTCCGCCTCCATAAGCACCCACATTGTTGGTGGCGATCAGGCGGACATCG CTGACTTTCCGTACCAGGTGTCCGTTCGCCTGGAGACCTACATGCTGCTCCAC ATCTGCGGTGGTAGCATCTATGCACCACGGGTCGTCATCACCGCCGCCCACTG CATCAAGGGACGCTATGCCTCGTACATCCGGATCGTGGCTGGTCAGAACTCG ATTGCCGATCTGGAGGAGCAGGGTGTTAAGGTCAGCAAACTGATCCCCCATG CCGGCTACAATAAGAAAACGTATGTGAATGATATCGGTTTGATCATCACTCG CGAGCCATTGGAGTACTCAGCCCTGGTGCAACCCATTGCTGTGGCCCTGGAG GCACCGCCGTCGGGTGCCCAGGCCGTTGTAAGTGGTTGGGGCAAGCGGGCTG AAGATGATGAAGCTCTGCCCGCCATGCTGCGCGCCGTTGAGCTGCAGATCAT CGAGAAGAGCACCTGCGGTGCCCAGTATCTGACCAAGGACTACACGGTGACC GATGAGATGCTCTGCGCCGGCTATCTGGAGGGCGGCAAGGACACCTGCAACG CTGGGGCGTGGGTTGCGGCAGGGAAGGATTCCCGGGTGTCTACACCAGCGTC AATTCCCATATCGATTGGATCGAAGAGCAGGCGGAGGCGTATCTCTAAAAAT GTGGATAGCTTCACAAGCACAACGCGAACAAATAAATCGAACAAATTATTAT TTTACCACAATAATAAATATGAAATGAGCATTTAGAAAACATGGTTTATAAT



ATATTTACAAATTAATATACGGTGTTTAACTCTTCATTTCAACTGGTTTTCCTA ATCAAAAACCTTTTTTATCTGACCATTACATTGGAATCTATAAGCCATTCTCG ACGATTTATATAAAAATAAAATTATTACCCAATTGGCATAGGTGAAGGCAAT TTATCTTGAGGAAGGGAAAAAGTACAATGTAACTAACCATAAATTTTATACT TTACAAAATCGTTTGATTGCATCATTTTAGAATAACTCAATGCAGAAATTAAA TTTATATTTGACTTGATGCAATCAAATAATATCCACAATATTAGAAATTTACC GTTTGCAGATAGTTTAACGTATTCGAGTAAGATTACATTTGTTTAAATCTTAA AAATTTAAAATAATTAGGAAGATTTTGTTTTTAAATATTAACGGCTTCTGGTA TTTTTTAGAGCTAGTATATACTTTCGTGGTAGACGTCGCTGGTATTTAAGCCA GTAAGATTCAGCCACACTGACAAAGAAAATATTCGTGAAAATTCTGCATACG GAAAGAAGAAAATTCGAGCAACAGAAAGCCAACACAATCCACAAAAATGTC TTTATTCGGAGCGTTGATGGGTGATTTCGACGACGATCTCGGCCTTATGAAGT AAGTACCAAATGGCGCAAAAAAAAAACTAAATAAATGCGGCTCGCCCCGCAG AAGCCCCATATATTTCCATACGTGTGCAGCTAACGAAGCCCTCTTGGGGCGTG GAAAAACAGCCAAATAATCGCAAAACAAGGTGTAAATCATTAATTGGCCCAT AGGCACACAATTAGGCCAATTAAACATATTTACGTGCCCAAAAATTAGCAAT GCGCAGCATGCGTGAAGTGAAGACGTAATAATCGATAATTTGAATCGAGCGA CCGCAGGGAAATGGAATTGGGGAAAATGCACTAGCAGGCGTTATTTCAAAGG TTTCGCCCTGTCACTGGGACTTTTGATAAGGCCCAACCGCAAAGTGACCCATG TAAAGGCAGGCTATCAGACCCTATTTTATGTATATACGTAGGCTACGCTGCCT TTATCACTATACTGCGATATTTGGCCACAAGTCATTTAGTTTGGCTTTGTTTAA AACTTAATTTCGGCTCAGTTTAAAATGAAACAAAAACGTAAAAGCAAATCAA ACCGTTCACAAATGGAGCTCCAGTAACTCGCACATCAGTCAAGTATCACTAA **GTTACTCATCTTTCGTTTGCAG**